

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: October 13, 2006, 01:10:07 ; Search time 200 Seconds
(without alignments)
16.003 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 7

Sequence: 1 YLTQPS 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2589679 seqs, 457216429 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2546695

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_8.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*
- 9: Geneseq2005s.*
- 10: Geneseq2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	8	ADQ16409 Amino aci
2	6	85.7	371	7	ADF04626 Bacterial
3	6	85.7	415	6	ADB08414 Alloiooc
4	6	85.7	503	6	ADB08416 Alloiooc
5	6	85.7	717	6	ADB08418 Alloiooc
6	6	85.7	1526	4	ABB63939 Drosophil
7	5	71.4	8	2	RAW57619 T-cell re
8	5	71.4	8	3	AAW88609 T-cell re
9	5	71.4	10	2	AAW25909 Beta-2-mi
10	5	71.4	10	4	AAU25775 Breast ca
11	5	71.4	21	9	ADU98146 mSlo1 cal
12	5	71.4	22	4	RAM17466 Peptide #
13	5	71.4	22	4	ABB36486 Peptide #
14	5	71.4	22	4	AAW29985 Peptide #
15	5	71.4	22	4	ABB31280 Peptide #
16	5	71.4	22	4	ABB21828 Protein #
17	5	71.4	22	4	RAM69651 Human bon
18	5	71.4	22	4	AAW57249 Human bra
19	5	71.4	22	4	ABG51333 Human liv
20	5	71.4	22	4	AAW05144 Peptide #
21	5	71.4	22	5	ABG39271 Human pep
22	5	71.4	41	7	ADB81615 Human ova
23	5	71.4	45	8	ADS07258 Staphyloc

24	5	71.4	50	8	ADU79042	Adu79042 Human pro
25	5	71.4	62	5	ABP04426	Abp04426 Human ORF
26	5	71.4	64	4	ABG06841	Abg06841 Novel hum
27	5	71.4	67	5	ABP10817	Abp10817 Human ORF
28	5	71.4	70	7	ABO66622	AbO66622 Klebsiell
29	5	71.4	78	4	AAW95241	Aam95241 Human rep
30	5	71.4	78	4	ABB95938	Abb95938 Human tes
31	5	71.4	81	4	ABG06812	Abg06812 Novel hum
32	5	71.4	92	4	AAW71384	Aag71384 Human gen
33	5	71.4	99	4	ABG22770	Abg22770 Novel hum
34	5	71.4	101	4	AAU63061	Aau63061 Propionib
35	5	71.4	101	6	ABM59580	Abm59580 Propionib
36	5	71.4	111	4	ABG19849	Abg19849 Novel hum
37	5	71.4	120	5	ABP43071	Abp43071 Human ova
38	5	71.4	122	8	ADY05847	Ady05847 Plant ful
39	5	71.4	129	4	AAW94957	Aab94957 Human pro
40	5	71.4	129	6	ABU00255	Abu00255 Human nov
41	5	71.4	129	8	ADRI4686	Adri4686 Human NF-
42	5	71.4	131	8	ADM87692	Adm87692 Human EST
43	5	71.4	134	4	AAU31384	Aau31384 Novel hum
44	5	71.4	134	6	ABO00449	AbO00449 Novel hum
45	5	71.4	134	8	ADX88163	Adx88163 Plant ful
46	5	71.4	135	3	AAU61631	Aag16191 Arabidops
47	5	71.4	144	4	AAU30881	Aau30881 Novel hum
48	5	71.4	146	4	AAW65762	Aag65762 Putative
49	5	71.4	146	7	ADP58647	Adp58647 Human pol
50	5	71.4	146	8	ABM81098	Abm81098 Tumour-as
51	5	71.4	146	8	ADY05516	Ady05516 Plant ful
52	5	71.4	150	8	ADR90527	Adr90527 Human ret
53	5	71.4	151	4	AAW91093	Aag91093 C glutami
54	5	71.4	151	9	AED71964	Aed71964 Corynebac
55	5	71.4	151	9	ABM51881	Abm51881 Human sec
56	5	71.4	162	8	ADW76620	Adw76620 Plant ful
57	5	71.4	163	7	ADD26756	Add26756 Human adi
58	5	71.4	164	3	AAW51880	Aab51880 Gene 2 hu
59	5	71.4	166	3	AAU33319	Aag13319 Arabidops
60	5	71.4	172	4	ADY64822	Ady64822 S. manson
61	5	71.4	176	9	ADW64822	Adw64822 Murine Rb
62	5	71.4	177	3	AAW53487	Aag53487 Arabidops
63	5	71.4	177	3	AAW08198	Aag08198 Arabidops
64	5	71.4	177	9	AED21447	Aed21447 Mouse-ear
65	5	71.4	177	9	AED61147	Aed61147 Thale cre
66	5	71.4	178	3	AAW27486	Aag27486 Arabidops
67	5	71.4	178	6	ABU43294	Abu43294 Protein e
68	5	71.4	191	3	AAU17534	Aau17534 Human sig
69	5	71.4	191	4	AAE13835	Aae13835 Human lun
70	5	71.4	191	4	AAE13835	Aae13835 Human lun
71	5	71.4	191	5	ABP39865	Abp39865 Staphyloc
72	5	71.4	191	7	ADD66701	Add66701 Human lun
73	5	71.4	191	7	ADW59337	Adw59337 Human pro
74	5	71.4	191	7	ADD45625	Add45625 Human pro
75	5	71.4	191	7	ADW87955	Adw87955 Human lun
76	5	71.4	191	8	ADS06905	Ads06905 Staphyloc
77	5	71.4	191	8	ABM81895	Abm81895 Tumour-as
78	5	71.4	191	8	ADS88276	Ads88276 Human pro
79	5	71.4	194	4	AAU17534	Aau17534 Human sig
80	5	71.4	194	4	AAU17111	Aau17111 Novel sig
81	5	71.4	194	4	ABW93819	Abw93819 Human nov
82	5	71.4	194	7	ADB94242	Adb94242 Human nov
83	5	71.4	200	8	ADR90533	Adr90533 Human ret
84	5	71.4	201	3	AAW53486	Aag53486 Arabidops
85	5	71.4	202	3	AAW53486	Aag53486 Arabidops
86	5	71.4	202	3	ADD26797	Add26797 Arabidops
87	5	71.4	204	8	ADM72128	Adm72128 Human NTR
88	5	71.4	207	8	ADR90538	Adr90538 Human ret
89	5	71.4	208	8	ADR90532	Adr90532 Human ret
90	5	71.4	211	3	AAW27485	Aag27485 Arabidops
91	5	71.4	219	4	ABB64552	Abb64552 Drosophil
92	5	71.4	224	2	AAW36516	Aaw36516 Human syn
93	5	71.4	224	2	AAW41709	Aay41709 Human pro
94	5	71.4	224	3	AAW40802	Aad40802 Human ORF
95	5	71.4	224	3	AAW44265	Aab44265 Human PRO
96	5	71.4	224	3	AAW24048	Aab24048 Human PRO

97	5	71.4	224	4	AAB64539	Aab64539	Gene 45 h	170	5	71.4	224	9	AED63934	Aed63934	Different
98	5	71.4	224	4	AAB64466	Aab64466	Human sec	171	5	71.4	225	7	ADP59585	Adp59585	Human pol
99	5	71.4	224	4	AAB64540	Aab64540	Human sec	172	5	71.4	225	7	ABM96257	Abm96257	M. xanthu
100	5	71.4	224	5	ABP03470	Abp03470	Human ORF	173	5	71.4	229	3	AAV74692	Aay74692	Neisseria
101	5	71.4	224	6	ABO25211	AbO25211	Novel hum	174	5	71.4	229	3	AAV74694	Aay74694	Neisseria
102	5	71.4	224	6	ABU72217	Abu72217	Novel hum	175	5	71.4	229	6	ABP79613	Abp79613	N. gonorr
103	5	71.4	224	6	ABU84897	Abu84897	Human sec	176	5	71.4	229	6	ABU37138	Abu37138	Protein e
104	5	71.4	224	6	ABU84897	Abu84897	Human sec	177	5	71.4	229	6	ABU38067	Abu38067	Protein e
105	5	71.4	224	6	ABU80364	Abu80364	Human sec	178	5	71.4	231	2	AAO4747	Aar04747	Amino aci
106	5	71.4	224	6	ADA24701	Ada24701	Novel hum	179	5	71.4	233	4	ABG22771	Abg22771	Novel hum
107	5	71.4	224	6	ABO19666	AbO19666	Novel hum	180	5	71.4	233	9	ABM95205	Abm95205	M. xanthu
108	5	71.4	224	6	ADA12362	Ada12362	Human sec	181	5	71.4	234	7	ADH89325	Adh89325	Z. maye 1
109	5	71.4	224	6	ABO19557	AbO19557	Novel hum	182	5	71.4	234	8	ADG44121	Adg44121	Z. maye 1
110	5	71.4	224	7	ADB73668	Abd73668	Human PRO	183	5	71.4	235	2	AAO4748	Aar04748	Amino aci
111	5	71.4	224	7	ADB76384	Abd76384	Human PRO	184	5	71.4	240	3	AAB43978	Aab43978	Human can
112	5	71.4	224	7	ADC43810	Adc43810	Human sec	185	5	71.4	241	3	AGG27706	Agg27706	Arabiidops
113	5	71.4	224	7	ADC61570	Adc61570	Human sec	186	5	71.4	241	3	AGG27706	Agg27706	Arabiidops
114	5	71.4	224	7	ADC63534	Adc63534	Human sec	187	5	71.4	242	8	ADS30131	AdS30131	Bacterial
115	5	71.4	224	7	ADC66634	Adc66634	Human sec	188	5	71.4	250	8	ADX72425	Adx72425	Plant ful
116	5	71.4	224	7	ADC68758	Adc68758	Human sec	189	5	71.4	254	2	AAV42165	Aay42165	Human che
117	5	71.4	224	7	ADC62818	Adc62818	Human sec	190	5	71.4	254	2	AAV42165	Aay42165	Human che
118	5	71.4	224	7	ADC67883	Adc67883	Human sec	191	5	71.4	254	3	AAB10491	Aab10491	Human CXC
119	5	71.4	224	7	ADC41203	Adc41203	Human sec	192	5	71.4	254	4	AAB34733	Aab34733	Human sec
120	5	71.4	224	7	ADC67258	Adc67258	Human sec	193	5	71.4	254	4	AAB68423	Aab68423	Amino aci
121	5	71.4	224	7	ADC62194	Adc62194	Human sec	194	5	71.4	254	4	AAB84199	Aab84199	Amino aci
122	5	71.4	224	7	ADC41827	Adc41827	Human sec	195	5	71.4	254	5	AAB84955	Aab84955	Human PRO
123	5	71.4	224	7	ADC45142	Adc45142	Human PRO	196	5	71.4	254	5	ABB95561	Abb95561	Human ang
124	5	71.4	224	7	ADE54986	Ade54986	Human PRO	197	5	71.4	254	7	ADD10567	Add10567	Human sec
125	5	71.4	224	7	ADE49196	Ade49196	Human sec	198	5	71.4	254	7	ADD11527	Add11527	Human sec
126	5	71.4	224	7	ADE35250	Ade35250	Human sec	199	5	71.4	254	7	ADD37320	Add37320	Human sec
127	5	71.4	224	7	ADE16364	Ade16364	Human sec	200	5	71.4	254	7	ADG87435	Adg87435	Human SEX
128	5	71.4	224	7	ADD72979	Add72979	Human sec	201	5	71.4	254	7	ADG87437	Adg87437	Human che
129	5	71.4	224	7	ADD72337	Add72337	Human sec	202	5	71.4	254	7	ADZ51814	Adz51814	Human sca
130	5	71.4	224	7	ADE16988	Ade16988	Human sec	203	5	71.4	254	8	ADZ51814	Adz51814	Human sca
131	5	71.4	224	7	ADF47002	Adf47002	Human sec	204	5	71.4	254	8	ADH43711	Adh43711	Human PRO
132	5	71.4	224	7	ADG52759	Adg52759	Human sec	205	5	71.4	258	8	ADK3056	Adk3056	Acinetoba
133	5	71.4	224	7	ADG60079	Adg60079	Human sec	206	5	71.4	261	4	AAB70543	Aab70543	Human PRO
134	5	71.4	224	7	ADI60839	Adi60839	Human sec	207	5	71.4	261	4	ABO01372	AbO01372	Human PRO
135	5	71.4	224	8	ADE84896	Ade84896	Human sec	208	5	71.4	261	6	ABO01373	AbO01373	Human PRO
136	5	71.4	224	8	ADE89597	Ade89597	Human sec	209	5	71.4	261	6	ABO01366	AbO01366	Human PRO
137	5	71.4	224	8	ADF61237	Adf61237	Human sec	210	5	71.4	261	8	ADN96118	AdN96118	Human NOV
138	5	71.4	224	8	ADF39929	Adf39929	Human sec	211	5	71.4	261	8	ADN96104	AdN96104	Human NOV
139	5	71.4	224	8	ADF45725	Adf45725	Human sec	212	5	71.4	261	8	ADN96116	AdN96116	Human NOV
140	5	71.4	224	8	ADF24121	Adf24121	Human sec	213	5	71.4	263	5	ABP39793	Abp39793	Staphyloc
141	5	71.4	224	8	ADF40553	Adf40553	Human sec	214	5	71.4	263	8	ADQ55572	AdQ55572	Staphyloc
142	5	71.4	224	8	ADF23497	Adf23497	Human sec	215	5	71.4	273	3	AAV57907	Aay57907	Human tra
143	5	71.4	224	8	ADF33480	Adf33480	Human sec	216	5	71.4	273	4	AAV57907	Aay57907	Human tra
144	5	71.4	224	8	ADF26947	Adf26947	Human sec	217	5	71.4	273	4	AAV57907	Aay57907	Human tra
145	5	71.4	224	8	ADF27583	Adf27583	Human sec	218	5	71.4	273	4	AAV57907	Aay57907	Human tra
146	5	71.4	224	8	ADF41177	Adf41177	Human sec	219	5	71.4	273	6	AAV57907	Aay57907	Human tra
147	5	71.4	224	8	ADF32856	Adf32856	Human sec	220	5	71.4	273	6	AAV57907	Aay57907	Human tra
148	5	71.4	224	8	ADF25222	Adf25222	Human sec	221	5	71.4	275	8	ADQ59517	AdQ59517	Human can
149	5	71.4	224	8	ADF26323	Adf26323	Human sec	222	5	71.4	279	4	AAV72625	Aay72625	Human ang
150	5	71.4	224	8	ADF34112	Adf34112	Human sec	223	5	71.4	290	7	ABO69586	AbO69586	Pseudomon
151	5	71.4	224	8	ADF46349	Adf46349	Human sec	224	5	71.4	291	6	ABP71288	Abp71288	Common re
152	5	71.4	224	8	ADG50335	Adg50335	Human sec	225	5	71.4	291	6	ABP71288	Abp71288	Common re
153	5	71.4	224	8	ADG49711	Adg49711	Human sec	226	5	71.4	297	6	ABP70972	Abp70972	Epoxide h
154	5	71.4	224	8	ADG51583	Adg51583	Human sec	227	5	71.4	297	6	ABP70972	Abp70972	Epoxide h
155	5	71.4	224	8	ADG49087	Adg49087	Human sec	228	5	71.4	297	6	ABP70972	Abp70972	Epoxide h
156	5	71.4	224	8	ADG48463	Adg48463	Human sec	229	5	71.4	300	6	ADA26915	Ada26915	Mouse the
157	5	71.4	224	8	ADG50959	Adg50959	Human sec	230	5	71.4	300	6	ADA26915	Ada26915	Mouse the
158	5	71.4	224	8	ADG58903	Adg58903	Human sec	231	5	71.4	302	3	AAV97213	Aay97213	Mouse PGC
159	5	71.4	224	8	ADG62359	Adg62359	Human sec	232	5	71.4	302	3	AAV97213	Aay97213	Mouse PGC
160	5	71.4	224	8	ADH25384	Adh25384	Human neu	233	5	71.4	302	6	ABJ18492	Abj18492	Campyloba
161	5	71.4	224	8	ADM17161	Adm17161	Human sec	234	5	71.4	302	6	ABJ18492	Abj18492	Campyloba
162	5	71.4	224	8	ADL06995	Adl06995	Human sec	235	5	71.4	303	6	ABU26594	Abu26594	Protein e
163	5	71.4	224	8	ADL91853	Adl91853	Human PRO	236	5	71.4	304	3	AAV97213	Aay97213	Mouse PGC
164	5	71.4	224	8	ADP54173	Adp54173	Human PRO	237	5	71.4	306	4	ABG69724	Abg69724	Arabiidops
165	5	71.4	224	8	ADT91094	Adt91094	Human PRO	238	5	71.4	310	6	ABU15108	Abu15108	Protein e
166	5	71.4	224	8	ADU50117	Adu50117	PRO615, S	239	5	71.4	312	4	AAV72968	Aay72968	Human oif
167	5	71.4	224	9	ADW49396	Adw49396	PRO615 pr	240	5	71.4	314	6	ABP75962	Abp75962	Human sec
168	5	71.4	224	9	ADZ52057	Adz52057	Human sec	241	5	71.4	317	6	ADA35598	Ada35598	Acinetoba
169	5	71.4	224	9	AED47885	Aed47885	Human PRO	242	5	71.4	320	6	ABP71289	Abp71289	Mouse the

GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: October 13, 2006, 01:20:08 ; Search time 186 Seconds
(without alignments)
17.433 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 7

Sequence: 1 YLTQPS 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2097797 seqs, 463214858 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2072432

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications AA.Main:

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	85.7	87	4	US-10-425-115-291176 Sequence 291176,
2	6	85.7	119	4	US-10-425-115-224207 Sequence 224207,
3	6	85.7	415	5	US-10-501-282-2354 Sequence 2354, Ap
4	6	85.7	503	5	US-10-501-282-2356 Sequence 2356, Ap
5	6	85.7	717	5	US-10-501-282-2358 Sequence 2358, Ap
6	6	85.7	1375	3	US-09-808-602-66 Sequence 66, Appl
7	6	85.7	1375	3	US-09-800-198-55 Sequence 55, Appl
8	6	85.7	1526	6	US-11-097-143-18609 Sequence 18609, A
9	5	71.4	10	3	US-09-827-345-8 Sequence 8, Appl
10	5	71.4	10	4	US-10-227-616-47 Sequence 47, Appl
11	5	71.4	10	6	US-11-220-407-8 Sequence 8, Appl
12	5	71.4	22	3	US-09-864-761-37126 Sequence 1726, A
13	5	71.4	41	5	US-10-487-561-104 Sequence 104, App
14	5	71.4	42	4	US-10-425-115-253500 Sequence 253500,
15	5	71.4	45	4	US-10-724-972A-6553 Sequence 6553, Ap
16	5	71.4	45	4	US-10-425-115-283377 Sequence 283377,
17	5	71.4	50	4	US-10-425-115-211966 Sequence 211966,
18	5	71.4	50	5	US-10-776-013-415 Sequence 415, App
19	5	71.4	51	4	US-10-424-599-206558 Sequence 206558,
20	5	71.4	53	4	US-10-425-115-215732 Sequence 215732,
21	5	71.4	55	4	US-10-437-963-129824 Sequence 129824,
22	5	71.4	55	4	US-10-425-115-311628 Sequence 311628,
23	5	71.4	56	4	US-10-437-963-204269 Sequence 204269,
24	5	71.4	64	5	US-10-450-763-37200 Sequence 37200, A
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28	5	71.4	67	4	US-10-425-115-325848 Sequence 325848,
29	5	71.4	69	4	US-10-425-115-337261 Sequence 337261,
30	5	71.4	70	4	US-10-424-599-162307 Sequence 162307,
31	5	71.4	71	4	US-10-425-115-260249 Sequence 260249,
32	5	71.4	72	4	US-10-425-115-262526 Sequence 262526,
33	5	71.4	73	4	US-10-425-115-251146 Sequence 251146,
34	5	71.4	74	4	US-10-425-115-200807 Sequence 200807,
35	5	71.4	75	4	US-10-425-115-303009 Sequence 303009,
36	5	71.4	76	4	US-10-425-115-302677 Sequence 302677,
37	5	71.4	77	4	US-10-425-115-236263 Sequence 236263,
38	5	71.4	78	3	US-09-764-891-3899 Sequence 3899, Ap
39	5	71.4	78	4	US-10-425-115-247760 Sequence 247760,
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OM protein - protein search, using sw model

Run on: October 13, 2006, 01:06:47 ; Search time 38 Seconds
(without alignments)
14.627 Million cell updates/sec

Title: US-10-537-648-1
Perfect score: 37
Sequence: 1 YLTQPOS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 295242 seqs, 79405279 residues

Total number of hits satisfying chosen parameters: 295242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications AA New.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	32	86.5	264	7	US-11-056-3558-116377
5	32	86.5	312	7	US-11-056-3558-37814
6	32	86.5	312	7	US-11-056-3558-105137
7	32	86.5	312	7	US-11-056-3558-116376
8	32	86.5	928	7	US-11-315-777-8
9	32	86.5	928	7	US-11-319-873-8
10	32	86.5	928	7	US-11-324-926-8
11	30	81.1	98	6	US-10-449-902-50568
12	30	81.1	303	6	US-10-449-902-30928
13	30	81.1	563	6	US-10-449-902-43710
14	30	81.1	563	6	US-10-449-902-53474
15	30	81.1	1013	6	US-10-449-902-45687
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21	29	78.4	228	7	US-11-056-3558-95156
22	29	78.4	293	6	US-10-526-572-17
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106	27	73.0	1352	6	US-10-511-302A-42	Sequence 42, Appl	179	26	70.3	836	6	US-11-313-104-16	Sequence 16, Appl
107	27	73.0	2359	6	US-10-543-503-134	Sequence 134, Appl	180	26	70.3	839	7	US-11-233-697-3261	Sequence 3261, Ap
108	26	70.3	112	7	US-11-292-414-12	Sequence 12, Appl	181	26	70.3	839	7	US-11-090-997-898	Sequence 898, App
109	26	70.3	113	7	US-11-337-300-321	Sequence 321, App	182	26	70.3	857	7	US-11-056-355B-70461	Sequence 70461, A
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112	26	70.3	173	7	US-11-192-046-66	Sequence 66, Appl	185	26	70.3	870	6	US-11-056-355B-46518	Sequence 46518, A
113	26	70.3	173	7	US-11-192-046-74	Sequence 74, Appl	186	26	70.3	879	6	US-10-540-898-258	Sequence 258, App
114	26	70.3	173	7	US-11-192-046-93	Sequence 93, Appl	187	26	70.3	918	6	US-10-449-902-47854	Sequence 47854, A
115	26	70.3	173	7	US-11-192-046-111	Sequence 111, App	188	26	70.3	949	7	US-11-056-355B-46517	Sequence 46517, A
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126	26	70.3	290	7	US-11-434-137-9880	Sequence 9880, Ap	199	26	70.3	1056	7	US-11-056-355B-46516	Sequence 46516, A
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128	26	70.3	290	7	US-11-434-199-9880	Sequence 9880, Ap	201	26	70.3	1122	6	US-10-540-898-260	Sequence 260, App
129	26	70.3	290	7	US-11-434-203-9880	Sequence 9880, Ap	202	26	70.3	1226	6	US-10-511-302A-16	Sequence 16, Appl
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131	26	70.3	307	7	US-11-434-137-2758	Sequence 2758, Ap	204	26	70.3	1356	6	US-10-480-962-16	Sequence 16, Appl
132	26	70.3	307	7	US-11-434-184-2758	Sequence 2758, Ap	205	26	70.3	1414	7	US-11-051-725-2	Sequence 2, Appl
133	26	70.3	307	7	US-11-434-199-2758	Sequence 2758, Ap	206	26	70.3	1420	7	US-11-051-725-122	Sequence 122, App
134	26	70.3	307	7	US-11-434-203-2758	Sequence 2758, Ap	207	26	70.3	1536	6	US-10-829-000-20	Sequence 20, Appl
135	26	70.3	311	6	US-10-471-571A-2418	Sequence 2418, Ap	208	26	70.3	1743	7	US-11-248-956-32	Sequence 32, Appl
136	26	70.3	319	7	US-11-330-403-5588	Sequence 5588, Ap	209	26	70.3	2347	7	US-11-051-725-1	Sequence 1, Appl
137	26	70.3	326	6	US-10-953-349-15560	Sequence 15560, Ap	210	26	70.3	2353	6	US-10-829-000-19	Sequence 19, Appl
138	26	70.3	326	6	US-11-056-355B-53527	Sequence 53527, A	211	26	70.3	2353	6	US-10-543-503-130	Sequence 130, App
139	26	70.3	369	6	US-10-449-902-36632	Sequence 36632, A	212	26	70.3	2353	6	US-11-051-725-119	Sequence 119, App
140	26	70.3	371	7	US-11-056-355B-9383	Sequence 9383, Ap	213	26	70.3	4834	6	US-10-505-928-827	Sequence 827, App
141	26	70.3	384	6	US-10-449-902-40368	Sequence 40368, A	214	25	67.6	22	7	US-11-300-563-12	Sequence 12, Appl
142	26	70.3	385	7	US-11-056-355B-9382	Sequence 9382, Ap	215	25	67.6	22	7	US-11-300-279-12	Sequence 12, Appl
143	26	70.3	386	7	US-11-249-111-92	Sequence 92, Appl	216	25	67.6	22	7	US-11-300-396-12	Sequence 12, Appl
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145	26	70.3	392	6	US-11-056-355B-53526	Sequence 53526, A	218	25	67.6	63	7	US-11-238-031-55	Sequence 5490, A
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148	26	70.3	428	6	US-10-449-902-44039	Sequence 44039, A	221	25	67.6	101	6	US-11-091-234A-25	Sequence 1006, Ap
149	26	70.3	441	6	US-10-953-349-15558	Sequence 15558, A	222	25	67.6	101	7	US-10-953-613C-1006	Sequence 26, Appl
150	26	70.3	441	6	US-11-056-355B-53525	Sequence 53525, A	223	25	67.6	110	7	US-11-091-234A-26	Sequence 26, Appl
151	26	70.3	449	7	US-11-056-355B-36484	Sequence 36484, A	224	25	67.6	110	6	US-10-540-084-4	Sequence 4, Appl
152	26	70.3	449	7	US-11-056-355B-104960	Sequence 104960, A	225	25	67.6	110	6	US-11-300-563-16	Sequence 16, Appl
153	26	70.3	449	7	US-11-056-355B-116199	Sequence 116199, A	226	25	67.6	110	7	US-11-300-279-16	Sequence 16, Appl
154	26	70.3	449	7	US-11-330-403-4084	Sequence 4084, Ap	227	25	67.6	110	7	US-11-300-279-16	Sequence 16, Appl
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156	26	70.3	468	6	US-10-449-902-36079	Sequence 36079, A	229	25	67.6	111	6	US-10-515-429-70	Sequence 70, Appl
157	26	70.3	468	6	US-11-330-403-1925	Sequence 1925, Ap	230	25	67.6	113	7	US-11-337-300-381	Sequence 381, App
158	26	70.3	472	6	US-10-669-920-1418	Sequence 1418, Ap	231	25	67.6	130	7	US-11-300-563-25	Sequence 25, Appl
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163	26	70.3	496	7	US-11-056-355B-94729	Sequence 94729, A	236	25	67.6	140	7	US-11-298-560-32	Sequence 32, Appl
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166	26	70.3	534	6	US-10-449-902-52090	Sequence 52090, A	239	25	67.6	158	7	US-11-249-111-85	Sequence 85, Appl
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168	26	70.3	611	7	US-11-293-697-4318	Sequence 4318, Ap	241	25	67.6	195	7	US-11-434-137-5998	Sequence 5998, Ap
169	26	70.3	619	6	US-10-449-902-56241	Sequence 56241, A	242	25	67.6	195	7	US-11-434-184-5998	Sequence 5998, Ap
170	26	70.3	677	7	US-11-056-355B-90972	Sequence 90972, A	243	25	67.6	195	7	US-11-434-199-5998	Sequence 5998, Ap
171	26	70.3	677	7	US-11-056-355B-94728	Sequence 94728, A	244	25	67.6	195	7	US-11-434-203-5998	Sequence 5998, Ap

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OM protein - protein search, using sw model

Run on: October 13, 2006, 00:54:56 ; Search time 199 Seconds
(without alignments)
16.083 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 37

Sequence: 1 YLTQPOS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database:

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9: Geneseq2005s.*

10: Geneseq2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	37	100.0	7	8	Adg16409 Amino aci
2	33	89.2	331	8	Adn18451 Bacterial
3	33	89.2	371	7	Adf04626 Bacterial
4	33	89.2	415	6	Adb08414 Alloiococ
5	33	89.2	503	6	Adb08416 Alloiococ
6	33	89.2	717	6	Adb08418 Alloiococ
7	32	86.5	250	8	Adr90527 Human ret
8	32	86.5	172	4	Abb66919 Murine Rb
9	32	86.5	200	8	Adr90533 Human ret
10	32	86.5	207	8	Adr90538 Human ret
11	32	86.5	208	8	Adr90532 Human ret
12	32	86.5	264	3	Aag42941 Arabidops
13	32	86.5	264	3	Aag05410 Arabidops
14	32	86.5	264	8	Adt56245 Plant pol
15	32	86.5	312	3	Aag42940 Arabidops
16	32	86.5	312	3	Aag05409 Arabidops
17	32	86.5	781	2	Aaw69369 Modified
18	32	86.5	781	6	Abus58789 Human ret
19	32	86.5	816	1	Aap82112 Human ret
20	32	86.5	816	2	Aar63584 Retinobla
21	32	86.5	816	2	Aar58568 Human ret
22	32	86.5	816	2	Aaw71355 Protein s
23	32	86.5	816	2	Aay01542 Human ret

24	32	86.5	816	6	ABUS8784	Human ret
25	32	86.5	832	2	AAW69368	Modified
26	32	86.5	832	2	ABUS8788	Human ret
27	32	86.5	851	2	AAW69370	Modified
28	32	86.5	851	2	AAW69367	Modified
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30	32	86.5	851	6	ABUS8787	Human ret
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33	32	86.5	871	2	AAW69375	Modified
34	32	86.5	871	6	ABUS8795	Human ret
35	32	86.5	874	6	AAW69366	Modified
36	32	86.5	874	6	ABUS8786	Human ret
37	32	86.5	895	2	AAW69365	Modified
38	32	86.5	895	6	ABUS8785	Human ret
39	32	86.5	897	2	AAW69371	Modified
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42	32	86.5	899	7	ADE56027	Rat Prote
43	32	86.5	899	7	ADE56023	Rat Prote
44	32	86.5	899	7	ADE56007	Rat Prote
45	32	86.5	899	7	ADE56011	Rat Prote
46	32	86.5	899	7	ADD48846	Rat Prote
47	32	86.5	899	7	ADE56019	Rat Prote
48	32	86.5	921	6	ABR43954	Mouse ret
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98	32	86.5	970	1	AAP90599	Aap90599 Human ret	171	29	78.4	224	6	ABO19666	Abol19666 Novel hum
99	31	83.8	66	4	AAU49143	Aau49143 Propionib	172	29	78.4	224	6	ADA12362	Ada12362 Human sec
100	31	83.8	66	6	ABM45662	Abm45662 Propionib	173	29	78.4	224	6	ABO19557	Abol19557 Novel hum
101	31	83.8	128	4	ABG02275	Abg02275 Novel hum	174	29	78.4	224	7	ADB73668	Adb73668 Human PRO
102	31	83.8	224	3	AAB40802	Aab40802 Human ORF	175	29	78.4	224	7	ADB76384	Adb76384 Human PRO
103	31	83.8	224	5	ABP03470	Abp03470 Human ORF	176	29	78.4	224	7	ADC43810	Adc43810 Human sec
104	31	83.8	339	6	ABU17118	Abu17118 Protein e	177	29	78.4	224	7	ADC61570	Adc61570 Human sec
105	31	83.8	361	6	ADA36646	Ada36646 Acinetoba	178	29	78.4	224	7	ADC63534	Adc63534 Human sec
106	31	83.8	508	8	ADQ67799	Adq67799 Novel hum	179	29	78.4	224	7	ADC66634	Adc66634 Human sec
107	31	83.8	549	7	ABO79802	Abol79802 Pseudomon	180	29	78.4	224	7	ADC68758	Adc68758 Human sec
108	31	83.8	562	5	ABP73802	Abp73802 Candida a	181	29	78.4	224	7	ADC62818	Adc62818 Human sec
109	31	83.8	714	4	AAG70834	Aag70834 C albican	182	29	78.4	224	7	ADC67883	Adc67883 Human sec
110	31	83.8	776	4	AAU41553	Aau41553 Propionib	183	29	78.4	224	7	ADC41203	Adc41203 Human sec
111	31	83.8	776	6	ABM38072	Abm38072 Propionib	184	29	78.4	224	7	ADC67258	Adc67258 Human sec
112	31	83.8	1047	4	ABM38072	Abm38072 Propionib	185	29	78.4	224	7	ADC62194	Adc62194 Human sec
113	30	81.1	162	8	ADX76620	Adx76620 Plant ful	186	29	78.4	224	7	ADC41827	Adc41827 Human sec
114	30	81.1	204	6	ADA36645	Ada36645 Acinetoba	187	29	78.4	224	7	ADD45142	Add45142 Human PRO
115	30	81.1	341	6	ADB06882	Adb06882 Alloioococ	188	29	78.4	224	7	ADE54986	Ades54986 Human PRO
116	30	81.1	345	6	ADB06884	Adb06884 Alloioococ	189	29	78.4	224	7	ADB49196	Adb49196 Human sec
117	30	81.1	421	7	ABO63138	Abol63138 Klebsiell	190	29	78.4	224	7	ADB35250	Adb35250 Human sec
118	30	81.1	437	8	ADX73491	Adx73491 Plant ful	191	29	78.4	224	7	ADB16364	Adb16364 Human sec
119	30	81.1	528	4	AAG81143	Aag81143 Mycobacte	192	29	78.4	224	7	ADD72979	Add72979 Human sec
120	30	81.1	528	6	ABU34906	Abu34906 Protein e	193	29	78.4	224	7	ADD72337	Add72337 Human sec
121	30	81.1	528	6	ABU36596	Abu36596 Protein e	194	29	78.4	224	7	ADE16988	Adel16988 Human sec
122	30	81.1	538	7	ADC61131	Adc61131 Baeyer-Vi	195	29	78.4	224	7	ADP47002	Adp47002 Human sec
123	30	81.1	553	9	ABP39586	Abp39586 L. pneumo	196	29	78.4	224	7	ADG52759	Adg52759 Human sec
124	30	81.1	574	9	ABE36163	Aeb36163 L. pneumo	197	29	78.4	224	7	ADI60839	Adi60839 Human sec
125	30	81.1	639	4	AAU71928	Aau71928 Human bon	198	29	78.4	224	8	ADE48496	Adel48496 Human sec
126	30	81.1	705	6	ABU49632	Abu49632 Protein e	199	29	78.4	224	8	ADE89597	Adel89597 Human sec
127	30	81.1	738	8	ADP99038	Adp99038 C. albica	200	29	78.4	224	8	ADP61237	Adp61237 Human sec
128	30	81.1	1200	3	AGG30768	Aag30768 Arabidops	201	29	78.4	224	8	ADP39929	Adp39929 Human sec
129	30	81.1	1207	3	AGG30767	Aag30767 Arabidops	202	29	78.4	224	8	ADP45725	Adp45725 Human sec
130	30	81.1	1215	3	AGB30766	Abg30766 Arabidops	203	29	78.4	224	8	ADP45725	Adp45725 Human sec
131	30	81.1	1526	4	ABE63933	Aeb63933 Drosophil	204	29	78.4	224	8	ADP24121	Adp24121 Human sec
132	29	78.4	10	2	AAU25909	Aau25909 Beta-2-mi	205	29	78.4	224	8	ADF40553	Adf40553 Human sec
133	29	78.4	10	4	AAU25775	Aau25775 Breast ca	206	29	78.4	224	8	ADF23497	Adf23497 Human sec
134	29	78.4	39	6	ABR47819	Abr47819 Human sec	207	29	78.4	224	8	ADP33480	Adp33480 Human sec
135	29	78.4	39	6	ABR00113	Abr00113 Human gen	208	29	78.4	224	8	ADP26947	Adp26947 Human sec
136	29	78.4	39	7	ABD91590	Abd91590 Human sec	209	29	78.4	224	8	ADP27583	Adp27583 Human sec
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140	29	78.4	49	5	ABP43160	Abp43160 Human ova	213	29	78.4	224	8	ADP34112	Adp34112 Human sec
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142	29	78.4	77	4	AAU99843	Aau99843 Human exc	215	29	78.4	224	8	ADG50335	Adg50335 Human sec
143	29	78.4	77	4	AAU42658	Aau42658 Human kid	216	29	78.4	224	8	ADG49711	Adg49711 Human sec
144	29	78.4	81	4	ABG06812	Abg06812 Novel hum	217	29	78.4	224	8	ADG51583	Adg51583 Human sec
145	29	78.4	89	4	ABG22770	Abg22770 Novel hum	218	29	78.4	224	8	ADG49087	Adg49087 Human sec
146	29	78.4	111	4	ABG19849	Abg19849 Novel hum	219	29	78.4	224	8	ADG48463	Adg48463 Human sec
147	29	78.4	134	8	ADX88163	Adx88163 Plant ful	220	29	78.4	224	8	ADG50959	Adg50959 Human sec
148	29	78.4	146	8	ADY05516	Ady05516 Plant ful	221	29	78.4	224	8	ADG50959	Adg50959 Human sec
149	29	78.4	153	8	ADG61779	Adg61779 Transcrip	222	29	78.4	224	8	ADG58903	Adg58903 Human sec
150	29	78.4	150	4	AAU18472	Aau18472 Human end	223	29	78.4	224	8	ADG62359	Adg62359 Human sec
151	29	78.4	162	3	ABE51881	Abe51881 Human sec	224	29	78.4	224	8	ADH25384	Adh25384 Human neu
152	29	78.4	184	3	ABU31880	Abu31880 Gene 2 hu	225	29	78.4	224	8	ADM17161	Adm17161 Human sec
153	29	78.4	178	6	AAU43294	Aau43294 Protein e	226	29	78.4	224	8	ADL06995	Adl06995 Human sec
154	29	78.4	187	8	ABP398953	Abp398953 Lung spec	227	29	78.4	224	8	ADL1853	Adl1853 Human PRO
155	29	78.4	191	5	ABP39865	Abp39865 Staphyloc	228	29	78.4	224	8	ADP54173	Adp54173 Human PRO
156	29	78.4	191	8	ADG06905	Adg06905 Staphyloc	229	29	78.4	224	8	ADU50194	Adu50194 Human PRO
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158	29	78.4	224	2	AAU36516	Aau36516 Human syn	231	29	78.4	224	9	ADW49396	Adw49396 PRO615 pr
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169	29	78.4	224	6	ABU80364	Abu80364 Human sec	242	29	78.4	224	9	ADW49396	Adw49396 PRO615 pr

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OM protein - protein search, using sw model

Run on: October 13, 2006, 01:05:12 ; Search time 52 Seconds
(without alignments)
11.783 Million cell updates/sec

Title: US-10-537-648-1
Perfect score: 37
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 1000 summaries

Database : Issued Patents_AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	32	86.5	816	1	US-08-038-760-3
3	32	86.5	816	1	US-08-470-091-3
4	32	86.5	928	1	US-08-504-329-1
5	32	86.5	928	1	US-08-959-638-8
6	32	86.5	928	1	US-08-482-627-5
7	32	86.5	928	2	US-08-801-092-4
8	32	86.5	928	2	US-08-328-673A-8
9	32	86.5	928	2	US-09-315-113-4
10	32	86.5	928	2	US-09-354-221-8
11	32	86.5	928	2	US-09-315-116-4
12	32	86.5	928	2	US-09-758-007-3
13	32	86.5	928	2	US-10-441-510-8
14	32	86.5	928	5	PCT-US94-10357-2
15	32	86.5	928	5	PCT-US94-10357-3
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17	31	83.8	324	2	US-09-248-796A-15950
18	31	83.8	361	2	US-09-328-352-7933
19	31	83.8	549	2	US-09-252-991A-28548
20	30	81.1	204	2	US-09-328-352-7932
21	30	81.1	421	2	US-09-489-039A-9655
22	30	81.1	455	2	US-09-248-796A-16498
23	30	81.1	528	2	US-09-712-363-194
24	30	81.1	681	2	US-09-270-767-42824
25	30	81.1	721	2	US-09-248-796A-16497
26	29	78.4	191	2	US-09-134-001C-4710

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28	78.4	224	2	US-09-999-833A-162	Sequence 162, App
29	78.4	224	2	US-10-020-445A-162	Sequence 162, App
30	78.4	224	2	US-09-978-189-162	Sequence 162, App
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32	78.4	224	3	US-10-145-129A-162	Sequence 162, App
33	78.4	224	3	US-10-013-929A-162	Sequence 162, App
34	78.4	224	3	US-10-013-917A-162	Sequence 162, App
35	78.4	356	2	US-09-949-016-10959	Sequence 10959, A
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39	78.4	357	5	PCT-US95-16806A-5	Sequence 5, Appli
40	78.7	70	2	US-09-489-039A-13139	Sequence 13139, A
41	78.7	73	2	US-09-655-270A-32	Sequence 32, Appl
42	78.7	151	2	US-09-605-703B-2140	Sequence 2140, Ap
43	78.7	183	2	US-09-248-796A-16520	Sequence 16520, A
44	78.7	191	2	US-09-854-133-393	Sequence 393, App
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57	78.7	303	3	US-10-303-128-29	Sequence 29, Appl
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59	78.7	317	2	US-09-328-352-6885	Sequence 6885, Ap
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61	78.7	348	2	US-09-134-001C-3294	Sequence 3294, Ap
62	78.7	352	2	US-09-328-352-4559	Sequence 4559, Ap
63	78.7	363	2	US-10-104-047-3425	Sequence 3425, Ap
64	78.7	408	2	US-09-949-016-9941	Sequence 9941, Ap
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66	78.7	451	2	US-09-902-540-13988	Sequence 13988, A
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82	78.7	730	3	US-10-013-917A-102	Sequence 102, App
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89	78.7	1196	2	US-09-275-252A-9	Sequence 9, Appli
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93	78.7	1262	2	US-09-519-076-22	Sequence 22, Appl
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95	73.0	94	2	US-09-149-476-505	Sequence 505, App
96	73.0	99	2	US-08-956-171E-5223	Sequence 5223, Ap
97	73.0	99	2	US-08-781-986A-5223	Sequence 5223, Ap
98	73.0	157	2	US-09-328-352-5951	Sequence 5951, Ap
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101	27	73.0	168	2	US-09-602-777A-88	Sequence 88, Appl	174	26	70.3	297	2	US-10-214-473-32	Sequence 32, Appl
102	27	73.0	173	2	US-09-248-796A-17745	Sequence 17745, A	175	26	70.3	306	2	US-09-584-568C-11	Sequence 11, Appl
103	27	73.0	180	2	US-09-270-767-44236	Sequence 44236, A	176	26	70.3	308	2	US-09-328-352-7061	Sequence 7061, Ap
104	27	73.0	220	2	US-09-252-991A-24796	Sequence 24796, A	177	26	70.3	335	2	US-09-489-039A-9285	Sequence 9285, Ap
105	27	73.0	233	2	US-09-902-540-14404	Sequence 14404, A	178	26	70.3	348	2	US-09-216-295-16	Sequence 16, Appl
106	27	73.0	243	2	US-09-270-767-33470	Sequence 33470, A	179	26	70.3	348	2	US-09-632-570-16	Sequence 16, Appl
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109	27	73.0	348	2	US-09-495-880A-13	Sequence 13, Appl	182	26	70.3	358	2	US-09-543-681A-4765	Sequence 4765, Ap
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111	27	73.0	348	2	US-09-495-880A-33	Sequence 33, Appl	184	26	70.3	386	2	US-09-724-623-92	Sequence 92, Appl
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113	27	73.0	358	2	US-09-248-796A-22578	Sequence 22578, A	186	26	70.3	387	2	US-10-288-930-92	Sequence 92, Appl
114	27	73.0	421	2	US-09-198-452A-535	Sequence 535, App	187	26	70.3	387	2	US-09-252-991A-22990	Sequence 22990, A
115	27	73.0	422	2	US-09-248-796A-16512	Sequence 16512, A	188	26	70.3	396	2	US-09-248-796A-20944	Sequence 20944, A
116	27	73.0	429	2	US-09-438-185A-497	Sequence 497, App	189	26	70.3	402	2	US-09-489-039A-13886	Sequence 13886, A
117	27	73.0	433	2	US-09-248-796A-24548	Sequence 24548, A	190	26	70.3	405	2	US-09-719-088B-3	Sequence 3, Appl
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120	27	73.0	503	2	US-09-583-110-4277	Sequence 4277, Ap	193	26	70.3	420	2	US-09-405-558-6	Sequence 6, Appl
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123	27	73.0	536	2	US-09-107-433-2945	Sequence 2945, Ap	196	26	70.3	441	2	US-09-248-796A-18617	Sequence 18617, A
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139	27	73.0	3801	1	US-08-822-445-10	Sequence 10, Appl	212	26	70.3	456	2	US-10-108-171A-2	Sequence 2, Appl
140	27	73.0	3801	2	US-09-396-540-10	Sequence 10, Appl	213	26	70.3	456	2	US-10-608-285A-27	Sequence 27, Appl
141	26	70.3	62	2	US-09-302-626B-32	Sequence 32, Appl	214	26	70.3	484	2	US-09-370-625A-27	Sequence 27, Appl
142	26	70.3	68	2	US-09-621-976-6132	Sequence 6132, Ap	215	26	70.3	484	2	US-09-557-800C-27	Sequence 27, Appl
143	26	70.3	86	2	US-09-302-626B-34	Sequence 34, Appl	216	26	70.3	484	2	US-09-370-625A-27	Sequence 27, Appl
144	26	70.3	88	2	US-09-543-681A-9203	Sequence 9203, Ap	217	26	70.3	488	2	US-09-919-039-33	Sequence 33, Appl
145	26	70.3	103	2	US-09-543-681A-5444	Sequence 5444, Ap	218	26	70.3	488	2	US-08-206-176-4	Sequence 4, Appl
146	26	70.3	124	2	US-09-640-211A-2157	Sequence 2157, Ap	219	26	70.3	491	1	US-08-206-176-4	Sequence 4, Appl
147	26	70.3	135	2	US-10-190-902B-5	Sequence 5, Appl	220	26	70.3	493	2	US-09-949-016-9617	Sequence 9617, Ap
148	26	70.3	146	2	US-10-104-047-2422	Sequence 2422, Ap	221	26	70.3	493	2	US-09-252-991A-21491	Sequence 21491, A
149	26	70.3	162	2	US-09-489-039A-7276	Sequence 7276, Ap	222	26	70.3	499	2	US-08-985-492-8	Sequence 8, Appl
150	26	70.3	184	2	US-09-489-039A-5522	Sequence 5522, Ap	223	26	70.3	500	3	US-09-277-401B-6	Sequence 6, Appl
151	26	70.3	185	2	US-09-134-000C-6497	Sequence 6497, Ap	224	26	70.3	506	2	US-09-328-352-7166	Sequence 7166, Ap
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163	4	57.1	107	US-11-281-266-40	Sequence 40, App	236	4	57.1	110	6	US-11-249-296-60	Sequence 60, App
164	4	57.1	107	US-11-056-3558-58422	Sequence 58422, A	237	4	57.1	110	6	US-11-249-296-62	Sequence 62, App
165	4	57.1	107	US-11-328-483-10	Sequence 10, App	238	4	57.1	110	6	US-11-249-296-78	Sequence 78, App
166	4	57.1	107	US-11-304-986-20	Sequence 20, App	239	4	57.1	110	6	US-11-337-300-321	Sequence 321, App
167	4	57.1	107	US-11-303-478-44	Sequence 44, App	240	4	57.1	110	6	US-11-337-300-349	Sequence 349, App
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Perfect score: 7

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Post-processing: Listing first 1000 summaries

Database : Issued Patents AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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119	4	57.1	6	2	US-09-308-237B-1	Sequence 11, Appl	192	4	57.1	43	1	US-08-777-192-37	Sequence 38, Appl
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143	4	57.1	13	2	US-08-505-250-7	Sequence 7, Appli	216	4	57.1	62	2	US-09-345-236B-18	Sequence 18, Appl
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Perfect score: 7

Sequence: 1 YUQPQS 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283334

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

PIR 80:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	85.7	290	2 A82236	pseudouridine synt
2	6	85.7	1375	2 T13822	frazzled gene prot
3	6	85.7	1526	2 T13823	frazzled gene prot
4	5	71.4	93	2 AF2346	hypothetical prote
5	5	71.4	135	2 G84469	probable glycine-r
6	5	71.4	157	2 T46440	hypothetical prote
7	5	71.4	177	2 G96794	probable calmoduli
8	5	71.4	193	2 T06972	hypothetical prote
9	5	71.4	206	2 H64022	hypothetical prote
10	5	71.4	214	2 S21969	19K zein precursor
11	5	71.4	220	2 S01838	nify protein - Kle
12	5	71.4	228	2 T49057	hypothetical prote
13	5	71.4	229	2 D83667	conserved hypothet
14	5	71.4	229	2 H83073	conserved hypothet
15	5	71.4	234	2 Z1ZM3	19K zein precursor
16	5	71.4	234	2 Z1ZMB1	19K zein precursor
17	5	71.4	234	2 S03417	19K zein precursor
18	5	71.4	239	2 T20603	hypothetical prote
19	5	71.4	249	2 J01981	lectin II - Scotch
20	5	71.4	253	2 T49820	hypothetical prote
21	5	71.4	258	2 H75436	conserved hypothet
22	5	71.4	284	2 S27843	homeotic protein s
23	5	71.4	291	2 D70080	transcription regu
24	5	71.4	295	2 A40587	probable transcrip
25	5	71.4	298	2 T52117	zinc finger protei
26	5	71.4	303	2 F81318	probable galactosy
27	5	71.4	303	2 T34112	hypothetical prote
28	5	71.4	310	2 E90867	hypothetical prote
29	5	71.4	310	2 D85751	hypothetical prote

30	5	71.4	310	2 B64882	conserved hypothet
31	5	71.4	318	2 AG7342	hypothetical prote
32	5	71.4	331	2 AG0072	probable MCCA-fam1
33	5	71.4	333	2 A81399	hypothetical prote
34	5	71.4	334	2 D5097	YgR protein - Eac
35	5	71.4	334	2 A38125	hypothetical prote
36	5	71.4	334	2 H85969	hypothetical prote
37	5	71.4	338	2 T47427	hypothetical prote
38	5	71.4	344	2 A80894	probable oxidoredu
39	5	71.4	348	2 D82252	Rnfp-related prote
40	5	71.4	379	2 JCS303	conserved hypothet
41	5	71.4	388	1 F64147	hypothetical prote
42	5	71.4	397	2 F20772	probable transamin
43	5	71.4	397	2 C86552	aspartate aminotra
44	5	71.4	402	2 B75297	diptidyl peptida
45	5	71.4	413	2 S73336	adhesin P1 precurs
46	5	71.4	426	2 T45800	UDP-N-acetylglucos
47	5	71.4	428	1 Q4ECAD	damX protein (arob
48	5	71.4	428	2 D86003	hypothetical prote
49	5	71.4	443	2 F91157	probable membrane
50	5	71.4	443	2 T10801	GDP dissociation i
51	5	71.4	450	2 D86717	hypothetical prote
52	5	71.4	455	2 H96797	hypothetical prote
53	5	71.4	460	2 A36555	unknown protein li
54	5	71.4	476	2 E83006	two-component resp
55	5	71.4	487	2 T29226	hypothetical prote
56	5	71.4	494	2 T42444	ID-myo-inositol-tr
57	5	71.4	517	2 E87613	pilus assembly pro
58	5	71.4	526	2 D96977	peptide chain rale
59	5	71.4	539	2 I49065	lymphoid-restrict
60	5	71.4	573	2 T00320	hypothetical prote
61	5	71.4	577	2 D91239	membrane protein l
62	5	71.4	577	2 A86087	hypothetical prote
63	5	71.4	577	2 F65202	hypothetical 66.6
64	5	71.4	613	2 A39552	oligoendopeptidase
65	5	71.4	634	1 S35574	transcription fact
66	5	71.4	645	2 T25824	hypothetical prote
67	5	71.4	654	2 T08600	hypothetical prote
68	5	71.4	690	2 H75469	conserved hypothet
69	5	71.4	783	2 JH0329	granulocyte colony
70	5	71.4	796	2 JG7355	peroxisome prolif
71	5	71.4	863	2 C38252	granulocyte colony
72	5	71.4	921	2 A33718	retinoblastoma pro
73	5	71.4	925	2 T00781	hypothetical prote
74	5	71.4	928	1 RBHU	retinoblastoma-ase
75	5	71.4	939	2 C70876	hypothetical prote
76	5	71.4	968	2 F84693	hypothetical prote
77	5	71.4	972	2 E84693	hypothetical prote
78	5	71.4	985	2 T27083	hypothetical prote
79	5	71.4	998	2 T30930	hypothetical prote
80	5	71.4	1009	2 T31081	cca3 protein - rat
81	5	71.4	1024	2 S38048	ubiquitin-protein
82	5	71.4	1097	2 T49187	hypothetical prote
83	5	71.4	1112	2 T30202	probable chitin sy
84	5	71.4	1113	2 S62904	calcium-regulated
85	5	71.4	1174	2 T43051	protein kinase C (
86	5	71.4	1175	2 JH0697	potassium channel
87	5	71.4	1184	2 A39800	calcium-activated
88	5	71.4	1184	2 I49017	calcium-activated
89	5	71.4	1189	2 S56852	hypothetical prote
90	5	71.4	1196	2 A48206	calcium-activated
91	5	71.4	1210	2 B64979	hypothetical 138.1
92	5	71.4	1226	2 E92328	s-methyltetrahydro
93	5	71.4	1467	2 T48162	hypothetical prote
94	5	71.4	4725	1 A44357	dysenin heavy chain
95	4	57.1	13	2 G61458	ig lamda chain V-
96	4	57.1	16	2 A45454	ankyrin-binding gl
97	4	57.1	21	2 B28835	ig heavy-chain v r
98	4	57.1	22	2 A37043	ig light chain, po
99	4	57.1	27	2 S00347	triacylglycerol li
100	4	57.1	27	2 B37043	ig heavy chain, po
101	4	57.1	27	2 A30323	amyloid protein AL
102	4	57.1	30	2 PL0189	ig light chain - s

103	4	57.1	30	2	S70341	176	4	57.1	100	2	E85677	unknown protein en
104	4	57.1	31	2	S77593	177	4	57.1	100	2	A98818	hypothetical prote
105	4	57.1	36	2	C37473	178	4	57.1	100	2	D87057	hypothetical prote
106	4	57.1	39	2	E86636	179	4	57.1	101	2	S10387	ig heavy chain V-D
107	4	57.1	49	2	G82678	180	4	57.1	101	2	B47624	ig heavy chain V-I
108	4	57.1	51	2	AB0546	181	4	57.1	101	2	T39075	hypothetical prote
109	4	57.1	54	2	AH1885	182	4	57.1	103	1	LIHUNM	ig lambda chain V-
110	4	57.1	57	2	A49111	183	4	57.1	103	2	S08462	ig heavy chain V r
111	4	57.1	61	1	DNVPBF	184	4	57.1	103	2	S36067	ig lambda chain -
112	4	57.1	61	2	C82536	185	4	57.1	104	2	T04149	phytochrome rice
113	4	57.1	62	2	AD2912	186	4	57.1	104	2	S36064	ig lambda chain -
114	4	57.1	64	2	T25247	187	4	57.1	105	2	S44124	ig lambda chain V
115	4	57.1	64	2	B97177	188	4	57.1	105	2	S52680	ribosomal protein
116	4	57.1	64	2	H98033	189	4	57.1	106	1	L4HUBU	ig lambda chain V-
117	4	57.1	64	2	H98046	190	4	57.1	106	1	L4HUKN	ig lambda chain V-
118	4	57.1	67	2	F81853	191	4	57.1	106	1	L4HUKN	ig lambda chain V-
119	4	57.1	69	2	JH0348	192	4	57.1	107	1	L4HUX	ig lambda chain V-
120	4	57.1	70	2	PC2063	193	4	57.1	107	1	L4HUXH	ig lambda chain V-
121	4	57.1	70	2	AH2112	194	4	57.1	107	2	B46516	ig lambda chain V
122	4	57.1	72	1	O38CFS	195	4	57.1	107	2	JH0347	T-cell receptor be
123	4	57.1	72	2	D85557	196	4	57.1	107	2	A82653	hypothetical prote
124	4	57.1	72	2	T12404	197	4	57.1	108	2	A12341	hypothetical prote
125	4	57.1	72	2	T11887	198	4	57.1	108	2	JN0695	tributylin chlori
126	4	57.1	73	2	AI0290	199	4	57.1	109	1	LIHUEP	ig lambda chain V-
127	4	57.1	73	2	AH2157	200	4	57.1	109	1	LIHUA	ig lambda chain V-
128	4	57.1	75	2	AB2497	201	4	57.1	109	1	L2HUBR	ig lambda chain V-
129	4	57.1	76	1	WSWL58	202	4	57.1	109	2	S68171	ig lambda chain V-
130	4	57.1	76	2	T44556	203	4	57.1	110	1	L2HUS8	ig lambda chain V-
131	4	57.1	77	2	JQ1295	204	4	57.1	110	2	S36258	ig lambda chain V-
132	4	57.1	78	2	B90778	205	4	57.1	110	2	S57428	ig light chain V-J
133	4	57.1	78	2	D70001	206	4	57.1	110	2	S57412	ig lambda chain V-
134	4	57.1	78	2	AH2386	207	4	57.1	110	2	S57408	ig lambda chain V-
135	4	57.1	80	2	F83467	208	4	57.1	110	2	S74442	ig lambda chain V-
136	4	57.1	80	2	AB2345	209	4	57.1	110	2	S51149	antibody light cha
137	4	57.1	81	2	I50975	210	4	57.1	110	2	G72597	hypothetical prote
138	4	57.1	81	2	I51144	211	4	57.1	111	1	LIHUNG	hypothetical prote
139	4	57.1	81	2	I51145	212	4	57.1	111	1	LIHUNW	ig lambda chain V-
140	4	57.1	84	2	D83940	213	4	57.1	111	1	LIHUNW	ig lambda chain V-
141	4	57.1	85	2	AF3548	214	4	57.1	111	1	LIHUNW	ig lambda chain V-
142	4	57.1	86	2	E81144	215	4	57.1	111	1	L2HUBH	ig lambda chain V-
143	4	57.1	86	2	S15229	216	4	57.1	111	1	L2HUBO	ig lambda chain V-
144	4	57.1	87	2	AD3551	217	4	57.1	111	1	L2HUNC	ig lambda chain V-
145	4	57.1	89	1	WMV2RF	218	4	57.1	111	1	L2HUNI	ig lambda chain V-
146	4	57.1	89	2	E98123	219	4	57.1	111	1	L2HUTG	ig lambda chain V-
147	4	57.1	89	2	AG3394	220	4	57.1	111	1	L2HUTR	ig lambda chain V-
148	4	57.1	90	2	C83960	221	4	57.1	111	1	L2HUVL	ig lambda chain V-
149	4	57.1	91	2	C90867	222	4	57.1	111	1	L2HUNW	ig lambda chain V-
150	4	57.1	91	2	AG3691	223	4	57.1	111	1	L6HULT	ig lambda chain V-
151	4	57.1	91	2	C97473	224	4	57.1	111	1	L6HUST	ig lambda chain V-
152	4	57.1	92	2	D64039	225	4	57.1	111	1	L7HUMT	ig lambda chain V-
153	4	57.1	93	2	AC3330	226	4	57.1	111	2	S46396	ig lambda chain V-
154	4	57.1	94	2	S72864	227	4	57.1	111	2	S19671	ig lambda chain -
155	4	57.1	94	2	S72920	228	4	57.1	111	2	S47185	VL lambda protein
156	4	57.1	95	2	S36065	229	4	57.1	111	2	S38499	ig lambda chain V1
157	4	57.1	96	2	S76170	230	4	57.1	111	2	S47009	ig lambda chain V
158	4	57.1	97	2	E53374	231	4	57.1	111	2	S36256	ig lambda chain V
159	4	57.1	97	2	I51216	232	4	57.1	111	2	S36263	ig lambda chain V
160	4	57.1	97	2	S10385	233	4	57.1	111	2	S46397	ig lambda chain V
161	4	57.1	97	2	S07266	234	4	57.1	111	2	S19673	ig lambda chain V
162	4	57.1	98	2	S36068	235	4	57.1	111	2	S36281	ig lambda chain V
163	4	57.1	98	2	S36047	236	4	57.1	111	2	S36274	ig lambda chain V
164	4	57.1	98	2	S36050	237	4	57.1	111	2	S38497	ig lambda chain -
165	4	57.1	98	2	S36046	238	4	57.1	111	2	S38497	ig lambda chain V-
166	4	57.1	98	2	S36048	239	4	57.1	112	1	LIHUNA	ig lambda chain V-
167	4	57.1	98	2	G69036	240	4	57.1	112	1	L2HUNG	ig lambda chain V-
168	4	57.1	99	2	S36053	241	4	57.1	112	1	L2HUNG	ig lambda chain V-
169	4	57.1	99	2	S36055	242	4	57.1	112	1	L6HUA	ig lambda chain V-
170	4	57.1	99	2	S36057	243	4	57.1	112	2	C44151	ig lambda chain V-
171	4	57.1	99	2	S36057	244	4	57.1	112	2	S46395	ig lambda chain V-
172	4	57.1	99	2	S36058	245	4	57.1	112	2	S44123	ig lambda chain V-
173	4	57.1	99	2	S36056	246	4	57.1	112	2	D44151	ig lambda chain V
174	4	57.1	99	2	S36054	247	4	57.1	112	2	A44151	ig lambda chain V
175	4	57.1	99	2	AD3031	248	4	57.1	112	2	S31515	ig lambda chain V

GenCore version 5.1.1.9
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OM protein - protein search, using sw model

Run on: October 13, 2006, 01:10:37 ; Search time 300 Seconds
(without alignments)
21.584 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 7

Sequence: 1 YLTQPS 7

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 92501592 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2849397

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : Uniprot 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	85.7	189	Q4SGH9	TETNG
2	6	85.7	192	KBR51	BRARE
3	6	85.7	216	Q6L17	PHOPR
4	6	85.7	227	P90610	TRIFO
5	6	85.7	230	Q4ZPB1	PSEU2
6	6	85.7	241	RLUE	VIBCH
7	6	85.7	362	1	RFPL RAT
8	6	85.7	453	Q4UPX1	THEAN
9	6	85.7	537	Q6NKA8	CORDI
10	6	85.7	546	Q3AVX9	SYNS9
11	6	85.7	562	Q349P1	RHOA
12	6	85.7	580	Q4SYV1	TEING
13	6	85.7	693	Q4UH42	THEAN
14	6	85.7	698	Q4NH83	THEPA
15	6	85.7	732	Q5E3M4	CHLAB
16	6	85.7	740	Q4HUY7	GIBZE
17	6	85.7	745	Q67PP5	SYNTH
18	6	85.7	877	Q54Y08	DICDI
19	6	85.7	1035	Q4H2B9	GIBZE
20	6	85.7	1136	Q6MEV2	PARUM
21	6	85.7	1137	Q8ML47	DRONE
22	6	85.7	1375	Q94537	DRONE
23	6	85.7	1526	Q94538	DRONE
24	6	85.7	1526	Q9V6D5	DRONE
25	5	71.4	13	Q9BDQ2	PANTR
26	5	71.4	45	Q3ME70	ANAVT
27	5	71.4	70	Q675B6	MOUSE
28	5	71.4	72	Q50370	MYCPN
29	5	71.4	75	Q6SJC8	9RHO
30	5	71.4	87	Q82V02	NITEU
31	5	71.4	91	Q322X6	SHIGBS

32	5	71.4	91	Q5N3U1	SYNP6
33	5	71.4	93	Q3MDN7	ANAVT
34	5	71.4	93	Q8YP75	ANASP
35	5	71.4	95	Q31QE7	SYNP7
36	5	71.4	95	Q3HB30	TRIER
37	5	71.4	99	Q8DMB0	SYNEL
38	5	71.4	107	Q2UV61	ASPOR
39	5	71.4	109	Q8CAF6	MOUSE
40	5	71.4	116	Q54XU9	DICDI
41	5	71.4	116	Q3CQ00	ALTAT
42	5	71.4	117	Q5TG33	FLAVE
43	5	71.4	117	Q3S819	9HIV1
44	5	71.4	122	Q4S617	TEING
45	5	71.4	128	Q8DHY7	SYNEP
46	5	71.4	129	Q9HAF6	HUMAN
47	5	71.4	129	Q3S807	9HIV1
48	5	71.4	132	Q6NKA8	CORDI
49	5	71.4	135	Q5N3U1	SYNP6
50	5	71.4	149	Q51676	PRCGU
51	5	71.4	149	Q70KA6	9ACTO
52	5	71.4	149	Q7SF68	NEUCR
53	5	71.4	145	Q5LTV3	SILPO
54	5	71.4	149	Q976D8	SULTO
55	5	71.4	149	Q2U7E7	ASPOR
56	5	71.4	150	Q6NEH8	CORDI
57	5	71.4	151	Q8NR47	CORGL
58	5	71.4	153	Q5BFY2	EMENI
59	5	71.4	155	Q76FB0	CYACA
60	5	71.4	155	Q44SE2	CHLLI
61	5	71.4	157	Q6JJ72	HUMAN
62	5	71.4	158	Q6MVK6	NEUCR
63	5	71.4	158	Q3LY92	RHOE4
64	5	71.4	162	Q2JMW3	9CYAN
65	5	71.4	162	Q2JXN5	9CYAN
66	5	71.4	162	Q7M7F7	GLOVI
67	5	71.4	167	Q3CSL5	ALTAT
68	5	71.4	168	Q2YHN3	PLAMU
69	5	71.4	175	Q2XCT6	PSEPU
70	5	71.4	175	Q6WPM5	ECOLI
71	5	71.4	177	Q77040	BOMMO
72	5	71.4	177	Q8LBV6	ARATH
73	5	71.4	177	Q5SRE6	ARATH
74	5	71.4	178	Q5HN44	STAEQ
75	5	71.4	178	Q65DP9	BACLD
76	5	71.4	178	Q8CNP8	STAES
77	5	71.4	184	Q4Q240	LEIMA
78	5	71.4	184	Q45AP2	9BURK
79	5	71.4	184	Q4LTP9	9BURK
80	5	71.4	185	Q8N7H9	HUMAN
81	5	71.4	185	Q7MMJ3	VIBVU
82	5	71.4	185	Q8DG02	VIBVU
83	5	71.4	186	Q2SH37	9GAMM
84	5	71.4	187	Q5ONB0	ENTHI
85	5	71.4	188	Q9CWU8	MOUSE
86	5	71.4	190	Q5LN40	SILPO
87	5	71.4	191	KBR52	CHICK
88	5	71.4	191	KBR52	HUMAN
89	5	71.4	191	KBR52	MOUSE
90	5	71.4	191	Q4SAK0	TEING
91	5	71.4	192	KBR52	BRARE
92	5	71.4	193	YCF21	CYAPA
93	5	71.4	196	Q2XV09	9GAMM
94	5	71.4	196	Q2ZVC9	SHEPU
95	5	71.4	202	Q44983	CAEEL
96	5	71.4	202	Q61CU1	CAEEL
97	5	71.4	202	Q853R2	9CAUD
98	5	71.4	203	Q3J5P6	RHO54
99	5	71.4	206	Y1244	HAETN
100	5	71.4	206	Q55J42	CRYNE
101	5	71.4	207	Q3FLZ1	9BURK
102	5	71.4	208	Q5B096	EMENI
103	5	71.4	208	Q30B81	9DEIN
104	5	71.4	208	Q41171	KINRA

Q5N3U1	synchococ
Q3MDN7	anabaena va
Q8YP75	anabaena sp
Q31QE7	synchococ
Q3HB30	trichodesmi
Q8DMB0	synchococ
Q2UV61	aspergillus
Q8CAF6	musculus
Q54XU9	dictyostell
Q3CQ00	pseudosalt
Q5TG33	flamulina
Q3S819	human immun
Q4S617	tetradon n
Q8DHY7	synchococ
Q9HAF6	homo sapien
Q3S807	human immun
Q6NKA8	corynebacte
Q5N3U1	arabidopsis
Q51676	pectinaria
Q70KA6	gordonia we
Q7SF68	neurospora
Q5LTV3	silicibacte
Q976D8	sulfolobus
Q2U7E7	aspergillus
Q6NEH8	corynebacte
Q8NR47	corynebacte
Q5BFY2	aspergillus
Q76FB0	cyanidium c
Q44SE2	chlorobium
Q6JJ72	homo sapien
Q6MVK6	neurospora
Q3LY92	rhodococcus
Q2JMW3	cyanobacter
Q2JXN5	cyanobacter
Q7M7F7	gloeobacter
Q3CSL5	pseudosalt
Q2YHN3	plantago ma
Q2XCT6	pseudomonas
Q6WPM5	escherichia
Q77040	bombyx mori
Q8LBV6	arabidopsis
Q5SRE6	arabidopsis
Q5HN44	staphylococ
Q65DP9	bacillus li
Q8CNP8	staphylococ
Q4Q240	leishmania
Q45AP2	burkholderi
Q4LTP9	burkholderi
Q8N7H9	homo sapien
Q7MMJ3	vibrio vuln
Q8DG02	vibrio vuln
Q2SH37	hahella che
Q5ONB0	entamoeba h
Q9CWU8	mus musculus
Q5LN40	silicibacte
Q5JW6	gallus gall
Q9N7Y9	homo sapien
Q9CR56	mus musculus
Q48AK0	tetradon n
Q6GJ12	brachydanio
P48358	cyanophora
Q2X0R0	shewanella
Q2ZVC9	shewanella
Q44983	caenorhabdi
Q61CU1	caenorhabdi
Q853R2	mycobacteri
Q3J5P6	rhodobacter
P44134	haemophilus
Q55J42	cryptococcu
Q3FLZ1	rhodoferrax
Q5B096	aspergillus
Q30B81	thermus sp.
Q41171	kineococcus

105	5	71.4	209	2	077039_BOMMO	077039_bombyx mori	178	5	71.4	279	2	088AQ3_PSESM	088AQ3_pseudomonas
106	5	71.4	209	2	051227_ENTHI	051227_entamoeba h	179	5	71.4	282	2	09RD75_STRCO	09RD75_streptomyces
107	5	71.4	209	2	030XA4_DESDG	030XA4_desulfobact	180	5	71.4	283	2	05RH54_BRARE	05RH54_brachydanio
108	5	71.4	211	2	0320C0_SHIBS	0320C0_shigella bo	181	5	71.4	284	1	SN0X5_SCHMA	SN0X5_schistosoma
109	5	71.4	212	2	0518A7_ENTHI	0518A7_entamoeba h	182	5	71.4	285	2	05AT53_EMENI	05AT53_aspergillus
110	5	71.4	212	2	070Y16_GIALA	070Y16_giardia lam	183	5	71.4	285	2	04AGR9_9CHLB	04AGR9_chlorobium
111	5	71.4	213	2	03B288_PELLD	03B288_peloidctyon	184	5	71.4	287	2	03IC24_PSEHT	03IC24_pseudoalter
112	5	71.4	214	2	041877_MAIZE	041877_zea mays (m	185	5	71.4	288	2	08X0N6_NEUCR	08X0N6_neurospora
113	5	71.4	215	1	Y1650_HAEDU	Y1650_haemophilus	186	5	71.4	289	2	048KA0_PSE14	048KA0_pseudomonas
114	5	71.4	216	2	05FQZ3_GLOOX	05FQZ3_gluconobact	187	5	71.4	289	2	073EP9_BACCI	073EP9_bacillus ce
115	5	71.4	218	2	03R021_RALME	03R021_ralstonia m	188	5	71.4	289	2	08JG31_CHICK	08JG31_gallus gall
116	5	71.4	218	2	04V0T4_BACCZ	04V0T4_bacillus ce	189	5	71.4	290	2	04HUM5_GIBZE	04HUM5_gibberella
117	5	71.4	219	2	09VQJ8_DROME	09VQJ8_drosophila	190	5	71.4	290	2	03GBD3_9FIRM	03GBD3_syntrophomo
118	5	71.4	222	2	05B8V3_EMENI	05B8V3_aspergillus	191	5	71.4	290	2	04ZU27_PSEU2	04ZU27_pseudomonas
119	5	71.4	223	2	07NE50_GLOVI	07NE50_gloeobacter	192	5	71.4	291	1	YXJO_BACSU	YXJO_bacillus su
120	5	71.4	224	1	SNZ2_HUMAN	SNZ2_homo sapien	193	5	71.4	292	2	0845T3_VIBVU	0845T3_vibrio vuln
121	5	71.4	227	2	08BNX8_MOUSE	08BNX8_mus muscucu	194	5	71.4	292	2	08DSB1_VIBVU	08DSB1_vibrio vuln
122	5	71.4	228	2	09LXV4_ARATH	09LXV4_arabidopsis	195	5	71.4	292	2	08E861_SHEON	08E861_shewanella
123	5	71.4	229	1	ISPD_NEIMA	091tm3_neisseria m	196	5	71.4	292	2	09PS77_CHICK	09PS77_gallus gall
124	5	71.4	229	1	ISPD_NEIMA	091ym4_neisseria m	197	5	71.4	293	2	05ZP99_9DELT	05ZP99_angiococcus
125	5	71.4	229	1	NIFY_KLEPN	P01335_klebsiella	198	5	71.4	294	2	02X611_SHEAMM	02X611_shewanella
126	5	71.4	229	2	Q5F829_NEIG1	Q5F829_neisseria g	199	5	71.4	294	2	02ZQ22_SHEPU	02ZQ22_syntrophoba
127	5	71.4	230	2	Q3KGM8_PSEPF	Q3KGM8_pseudomonas	200	5	71.4	294	2	Q3N3N5_9DELT	Q3N3N5_syntrophoba
128	5	71.4	230	2	Q4KGS5_PSEF5	Q4KGS5_pseudomonas	201	5	71.4	295	1	RPSC_MYXXX	RPSC_myxococcus
129	5	71.4	230	2	Q3V3H7_MOUSE	Q3V3H7_mus muscucu	202	5	71.4	295	2	08J2Q9_GIBMO	08J2Q9_gibberella
130	5	71.4	234	1	ZEAL_MAIZE	P02859_zea mays (m	203	5	71.4	295	2	07VVS9_BORDERP	07VVS9_bordetella
131	5	71.4	234	1	ZEAL_MAIZE	P06675_zea mays (m	204	5	71.4	295	2	07W7A4_BORDERP	07W7A4_bordetella
132	5	71.4	234	1	ZEAS_MAIZE	P08416_zea mays (m	205	5	71.4	295	2	07WKP1_BORDERP	07WKP1_bordetella
133	5	71.4	234	2	Q946V6_MAIZE	Q946V6_zea mays (m	206	5	71.4	295	2	Q4K9M0_PSEF5	Q4K9M0_pseudomonas
134	5	71.4	234	2	Q4AXJ9_9BURK	Q4AXJ9_polaromonas	207	5	71.4	297	2	06BMJ9_DEBHA	06BMJ9_debaryomyces
135	5	71.4	235	2	067E24_9TEHT	067E24_beryx splen	208	5	71.4	298	2	064936_ARATH	064936_arabidopsis
136	5	71.4	237	2	Q31KM9_PSEHT	Q31KM9_pseudoalter	209	5	71.4	298	2	07MCB2_VIBVU	07MCB2_vibrio vuln
137	5	71.4	239	2	Q9XVA0_CABEL	Q9XVA0_caenorhabdi	210	5	71.4	299	2	Q4HSD9_9DEIO	Q4HSD9_deinococcus
138	5	71.4	240	2	Q4CHF5_CLOTM	Q4CHF5_clostridium	211	5	71.4	299	2	Q3K9Y5_PSEPF	Q3K9Y5_pseudomonas
139	5	71.4	242	2	Q2J5U5_9ACTO	Q2J5U5_franksia sp.	212	5	71.4	300	1	RNH3_CHUCV	RNH3_chlamydomoni
140	5	71.4	246	2	Q88YR6_LACPL	Q88YR6_lactobacill	213	5	71.4	300	2	Q2W9G6_MAGSA	Q2W9G6_magnetospir
141	5	71.4	248	1	LEC2_CVTSC	P29257_cytisus sco	214	5	71.4	300	2	Q3C6U8_9CLOT	Q3C6U8_alkaliphilu
142	5	71.4	248	2	Q4H9K4_9DEIO	Q4H9K4_deinococcus	215	5	71.4	300	2	05HVN7_CAMJR	05HVN7_campylobact
143	5	71.4	249	2	Q890D4_LACPL	Q890D4_lactobacill	216	5	71.4	301	2	082S42_NITEU	082S42_nitrosomona
144	5	71.4	249	2	Q890D5_BRAJA	Q890D5_bradyrhizob	217	5	71.4	302	2	050M40_ENTHI	050M40_entamoeba h
145	5	71.4	250	2	Q4DLB2_TRYCR	Q4DLB2_trypanosoma	218	5	71.4	302	2	087189_VIBPA	087189_vibrio para
146	5	71.4	250	2	Q517R9_ENTHI	Q517R9_entamoeba h	219	5	71.4	303	2	09PNF5_CAMJE	09PNF5_campylobact
147	5	71.4	251	2	Q2SYPB_BURTH	Q2SYPB_burkholderi	220	5	71.4	304	2	02T2C7_BURTH	02T2C7_burkholderi
148	5	71.4	252	2	Q2U0E8_ASPOR	Q2U0E8_aspergillus	221	5	71.4	304	2	082S45_NITEU	082S45_nitrosomona
149	5	71.4	252	2	Q4DEC9_TRYCR	Q4DEC9_trypanosoma	222	5	71.4	306	2	09VGJ4_DROME	09VGJ4_drosophila
150	5	71.4	254	1	SCYBG_HUMAN	Q9H2A7_homo sapien	223	5	71.4	306	2	Q83LA7_SHIFL	Q83LA7_shigella fl
151	5	71.4	254	2	Q7Q9R3_ANOGA	Q7Q9R3_anopheles g	224	5	71.4	307	2	Q3XNH2_9PROT	Q3XNH2_magnetococc
152	5	71.4	256	2	Q8XYM8_RALSO	Q8XYM8_ralstonia s	225	5	71.4	310	1	YCJY_ECOLI	YCJY_escherichia
153	5	71.4	258	2	Q7VIA4_HELHP	Q7VIA4_helicobacte	226	5	71.4	310	2	05QPJ1_HUMAN	05QPJ1_homo saplen
154	5	71.4	258	2	Q8PGV5_SYNEL	Q8PGV5_synecococc	227	5	71.4	310	2	054G80_DICDI	054G80_dictyosteli
155	5	71.4	258	2	Q9RVC8_DEIRA	Q9RVC8_deinococcus	228	5	71.4	310	2	Q3Z177_SHISS	Q3Z177_shigella so
156	5	71.4	260	2	Q8KKW8_RHRET	Q8KKW8_rhizobium e	229	5	71.4	310	2	08X8M5_ECO57	08X8M5_escherichia
157	5	71.4	260	2	Q6DBF6_ERWCT	Q6DBF6_erwinia car	230	5	71.4	310	2	08FHQ8_ECOL6	08FHQ8_escherichia
158	5	71.4	261	2	Q9N3Z9_CABEL	Q9N3Z9_caenorhabdi	231	5	71.4	311	2	04FXB8_LEIMA	04FXB8_leishmania
159	5	71.4	261	2	Q4L9Q9_STAHO	Q4L9Q9_staphylococ	232	5	71.4	311	2	04LY78_9BURK	04LY78_burkholderi
160	5	71.4	261	2	Q5HKP4_STAEO	Q5HKP4_staphylococ	233	5	71.4	311	2	03J346_BURS3	03J346_burkholderi
161	5	71.4	261	2	Q8CTU9_STAES	Q8CTU9_staphylococ	234	5	71.4	311	2	Q3QV37_9RHOB	Q3QV37_silicibacte
162	5	71.4	264	2	Q3H314_9ACTO	Q3H314_nocardioide	235	5	71.4	312	2	Q3ZHW7_THIDE	Q3ZHW7_thiobacillu
163	5	71.4	264	2	Q87B53_XYLFT	Q87B53_xyliella fas	236	5	71.4	313	2	Q3SMF8_THIDA	Q3SMF8_thiobacillu
164	5	71.4	266	2	Q43J76_9CHLB	Q43J76_chlorobium	237	5	71.4	313	2	Q3AWGO_SYNS9	Q3AWGO_synecococc
165	5	71.4	270	2	Q3LIG2_MOUSE	Q3LIG2_mus muscucu	238	5	71.4	314	2	044JEB_CHRSL	044JEB_chromohalob
166	5	71.4	270	2	Q9PUVA_9PERC	Q9PUVA_channa sp.	239	5	71.4	314	2	02QFL5_EHRCH	02QFL5_ehrlichia c
167	5	71.4	270	2	Q9PFW3_ZEUPA	Q9PFW3_zeus faber	240	5	71.4	316	2	Q3IKU7_PSEHT	Q3IKU7_pseudoalter
168	5	71.4	271	2	Q4NKF3_9MICC	Q4NKF3_arthrobacte	241	5	71.4	317	2	Q3WMD7_9RHIZ	Q3WMD7_mesorhizobi
169	5	71.4	272	2	Q604A3_METCA	Q604A3_methylococc	242	5	71.4	317	2	Q5SM20_THET8	Q5SM20_thermus the
170	5	71.4	273	2	Q8ZSP1_PYRAE	Q8ZSP1_pyrobaculum	243	5	71.4	317	2	Q72GH7_THET2	Q72GH7_thermus the
171	5	71.4	273	2	Q6C124_YARLI	Q6C124_yarrowia li	244	5	71.4	317	2	Q2T3V5_BURTH	Q2T3V5_burkholderi
172	5	71.4	274	2	Q2ITD2_RHOPA	Q2ITD2_rhodopseudo	245	5	71.4	318	2	Q3JUG8_BURP1	Q3JUG8_burkholderi
173	5	71.4	275	2	Q3KQZ2_HUMAN	Q3KQZ2_homo sapien	246	5	71.4	318	2	Q6ZAE1_BURMA	Q6ZAE1_burkholderi
174	5	71.4	276	2	Q825N2_STRAW	Q825N2_streptomyce	247	5	71.4	318	2	Q63N00_BURPS	Q63N00_burkholderi
175	5	71.4	277	2	Q5E8W7_VIBF1	Q5E8W7_vibrio fisc	248	5	71.4	318	2	09AA52_CAUCR	09AA52_caulobacter
176	5	71.4	277	2	Q7NHM8_GLOVI	Q7NHM8_gloeobacter	249	5	71.4	318	2		
177	5	71.4	279	2			250	5	71.4	318	2		

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OM protein - protein search, using sw model

Run on: October 13, 2006, 01:00:06 ; Search time 41 Seconds
(without alignments)
16.427 Million cell updates/sec

Title: US-10-537-648-1
Perfect score: 37
Sequence: 1 YLTQPS 7

Scoring table: BLOSUM62
Gapop 10.0 , Capext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	89.2	331	2 F69025	ATP phosphoribosyl
2	32	86.5	264	2 B71448	hypothetical prote
3	32	86.5	539	2 I49065	lymphoid-restrict
4	32	86.5	921	2 A33718	retinoblastoma pro
5	32	86.5	928	1 RBHU	retinoblastoma-as
6	31	83.8	294	2 S27843	homeotic protein s
7	31	83.8	538	2 B83525	probable gamma-glu
8	30	81.1	230	2 A82326	pseudouridine synt
9	30	81.1	528	2 G70055	probable choline d
10	30	81.1	645	2 T25824	hypothetical prote
11	30	81.1	705	2 B82044	guanosine-3',5'-bi
12	30	81.1	980	2 T49570	hypothetical prote
13	30	81.1	1205	2 C84848	hypothetical prote
14	30	81.1	1375	2 T13822	frazzled gene prot
15	30	81.1	1483	2 T19751	hypothetical prote
16	30	81.1	1526	2 T13823	frazzled gene prot
17	29	78.4	214	2 S21969	19K zein precursor
18	29	78.4	229	2 T33141	hypothetical prote
19	29	78.4	234	1 ZIZN3	19K zein precursor
20	29	78.4	234	1 ZIZMB1	19K zein precursor
21	29	78.4	234	2 S03417	19K zein precursor
22	29	78.4	248	2 AB1941	hypothetical prote
23	29	78.4	263	2 A54543	beta-lactamase (EC
24	29	78.4	263	2 S23929	beta-lactamase (EC
25	29	78.4	231	2 S42075	beta-lactamase (EC
26	29	78.4	294	2 S19006	beta-lactamase (EC
27	29	78.4	327	2 T34562	G protein pathway
28	29	78.4	382	1 MFN241	matrix protein - s
29	29	78.4	402	2 B75297	dipeptidyl peptida

30	29	78.4	450	2 D86717	hypothetical prote
31	29	78.4	460	2 A96555	unknown protein [i
32	29	78.4	466	2 S75657	coproporphyrinogen
33	29	78.4	578	2 S74578	probable flavoprot
34	29	78.4	612	2 E64820	probable oligopept
35	29	78.4	612	2 D90742	hypothetical prote
36	29	78.4	612	2 G85592	hypothetical prote
37	29	78.4	613	2 T09105	holocytochrome c-t
38	29	78.4	637	2 S75772	hypothetical prote
39	29	78.4	1883	2 G82875	hypothetical prote
40	28	75.7	75	2 S36422	retrovirus-related
41	28	75.7	81	2 T15040	RNA-directed DNA p
42	28	75.7	81	2 T10743	RNA-directed DNA p
43	28	75.7	89	2 C47759	retrovirus-related
44	28	75.7	138	2 A29479	thyrotropin beta c
45	28	75.7	146	2 S36970	hypothetical prote
46	28	75.7	157	2 T16140	hypothetical prote
47	28	75.7	193	2 T66972	hypothetical prote
48	28	75.7	206	2 H64022	hypothetical prote
49	28	75.7	239	2 T20603	hypothetical prote
50	28	75.7	241	2 A04048	4-diphosphocytidyl
51	28	75.7	245	2 G64471	cell division prot
52	28	75.7	253	2 T49820	hypothetical prote
53	28	75.7	291	2 D70080	transcription regu
54	28	75.7	292	2 T03085	ribonuclease homol
55	28	75.7	303	2 F81318	probable galactosy
56	28	75.7	303	2 T34112	hypothetical prote
57	28	75.7	308	2 AC1867	hypothetical prote
58	28	75.7	310	2 E90867	hypothetical prote
59	28	75.7	310	2 D85751	hypothetical prote
60	28	75.7	310	2 B64882	conserved hypothet
61	28	75.7	318	2 G87342	hypothetical prote
62	28	75.7	333	2 A81399	hypothetical prote
63	28	75.7	338	2 T47427	hypothetical prote
64	28	75.7	426	2 T45800	UDP-N-acetylglucos
65	28	75.7	443	2 T10801	GDP dissociation i
66	28	75.7	515	1 IQMCL	replication initia
67	28	75.7	517	2 E87613	pilus assembly pro
68	28	75.7	547	2 JC7539	beta-glucosidase (
69	28	75.7	573	2 T00320	hypothetical prote
70	28	75.7	577	2 D91239	membrane protein [
71	28	75.7	577	2 A86087	hypothetical prote
72	28	75.7	577	2 F52202	hypothetical 66.6
73	28	75.7	632	2 H70339	NADH2 dehydrogenas
74	28	75.7	661	2 T46364	hypothetical prote
75	28	75.7	722	2 T26297	hypothetical prote
76	28	75.7	769	2 F85077	probable transposo
77	28	75.7	815	2 B30843	glutenin high mole
78	28	75.7	815	2 JN0689	glutenin, high-mol
79	28	75.7	830	2 S15720	glutenin high mole
80	28	75.7	838	1 EEWTHW	glutenin, high mol
81	28	75.7	848	2 S02262	glutenin high mole
82	28	75.7	853	2 T46347	hypothetical prote
83	28	75.7	874	2 I64095	alanine-tRNA ligas
84	28	75.7	919	2 S45298	retinoblastoma-ass
85	28	75.7	925	2 T00781	hypothetical prote
86	28	75.7	939	2 C70876	hypothetical prote
87	28	75.7	950	2 E64135	reverse transcript
88	28	75.7	964	2 T01860	hypothetical prote
89	28	75.7	985	2 T27083	oxoglutarate dehyd
90	28	75.7	990	2 JC7878	hypothetical prote
91	28	75.7	1024	2 S38048	fucokinase (EC 2.7
92	28	75.7	1113	2 S62904	ubiquitin-protein
93	28	75.7	1139	2 A49370	calcium-regulated
94	28	75.7	1175	2 JH0697	BLA-associated cyc
95	28	75.7	1184	2 A39800	calcium-activated
96	28	75.7	1184	2 I49017	calcium-activated
97	28	75.7	1196	2 A48206	calcium-activated
98	28	75.7	1199	2 S20969	Na+/Ca2+,K+-exchan
99	28	75.7	1447	2 F82909	hypothetical prote
100	28	75.7	2241	2 S09811	hypothetical prote
101	28	75.7	7829	2 T15789	hypothetical prote
102	28	75.7	9376	2 T14593	synergomycin synth

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OM protein - protein search, using sw model

Run on: October 13, 2006, 01:05:31 ; Search time 187 Seconds
(without alignments)
17.340 Million cell updates/sec

Title: US-10-537-648-1
Perfect score: 37
Sequence: 1 YLTQPS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celella_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celella_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celella_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celella_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celella_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celella_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	89.2	87	4	US-10-425-115-291176
2	33	89.2	119	4	US-10-425-115-224207
3	33	89.2	251	4	US-10-319-799-68
4	33	89.2	331	4	US-10-369-493-1104
5	33	89.2	415	5	US-10-501-282-2354
6	33	89.2	503	5	US-10-501-282-2356
7	33	89.2	717	5	US-10-501-282-2358
8	32	86.5	264	5	US-10-739-930-6332
9	32	86.5	781	3	US-09-469-522-37
10	32	86.5	815	5	US-10-732-923-15103
11	32	86.5	816	3	US-09-469-522-4
12	32	86.5	832	3	US-09-469-522-35
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14	32	86.5	851	3	US-09-469-522-39
15	32	86.5	869	3	US-09-469-522-47
16	32	86.5	871	3	US-09-469-522-49
17	32	86.5	874	3	US-09-469-522-31
18	32	86.5	882	5	US-10-732-923-15123
19	32	86.5	895	3	US-09-469-522-29
20	32	86.5	897	3	US-09-469-522-41
21	32	86.5	899	5	US-10-732-923-15104
22	32	86.5	921	5	US-10-492-901-11
23	32	86.5	921	5	US-10-732-923-15102
24	32	86.5	928	3	US-09-758-007-3
25	32	86.5	928	3	US-09-860-211-8
26	32	86.5	928	3	US-09-469-522-2
27	32	86.5	928	3	US-09-469-522-51

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29	86.5	928	3	US-09-860-286-8	Sequence 8, Appli
30	86.5	928	4	US-10-028-726-2	Sequence 2, Appli
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44	83.8	228	4	US-10-767-701-32911	Sequence 32911, A
45	83.8	339	4	US-10-282-122A-45042	Sequence 45042, A
46	83.8	562	4	US-10-032-585-7639	Sequence 7639, Ap
47	83.8	1047	6	US-11-097-143-29241	Sequence 29241, A
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53	81.1	345	5	US-10-501-282-824	Sequence 824, App
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61	81.1	705	4	US-10-282-122A-77556	Sequence 77556, A
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 12, 2006, 21:41:10 ; Search time 148 Seconds
(without alignments)
132.560 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 7

Sequence: 1 YLTQPS 7

Scoring table: OLIGO
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Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 2395520 seqs, 934235491 residues

Word size: 1

Total number of hits satisfying chosen parameters: 4785881

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	6	85.7	48	7	US-11-434-199-11221
6	6	85.7	48	7	US-11-434-203-11221
7	6	85.7	181	8	US-11-266-748A-425888

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576	85.7	6	8	576	6	US-10-533-365-139	Sequence 139, App
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590	85.7	6	8	590	8	US-11-266-748A-137324	Sequence 137324, A
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752	85.7	6	8	752	8	US-11-266-748A-346700	Sequence 346700, A
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 12, 2006, 20:39:59 ; Search time 2564 Seconds

(without alignments)
261.875 Million cell updates/sec

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Listing first 1000 summaries

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15: gb_ba: +

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	37	100.0	103836	6	AC125670	AC125670 Rattus no
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14	37	100.0	135924	14	AC163264	AC163264 Rhinoloph
15	37	100.0	137877	12	AC167095	AC167095 Sorex ara
16	37	100.0	139969	12	AC170718	AC170718 Atelerix
17	37	100.0	144819	12	AC173446	AC173446 Atelerix
18	37	100.0	148743	11	BX324154	BX324154 Zebrafish
19	37	100.0	151772	6	AC109294	AC109294 Mus muscu
20	37	100.0	155624	5	AC027058	AC027058 Homo sapi
21	37	100.0	165228	5	CNS01DWS	AL138479 Human chr
22	37	100.0	166758	12	AC173466	AL173466 Sorex ara
23	37	100.0	167388	12	AC157445	AC157445 Sus scrof
24	37	100.0	170875	6	AC154429	AC154429 Mus muscu
25	37	100.0	172427	5	AC161282	AC161282 Pan trogl
26	37	100.0	172853	5	AC084361	AC084361 Homo sapi
27	37	100.0	173555	4	AP003277	AP003277 Oryza sat
28	37	100.0	179085	5	AC175825	AC175825 Pan trogl
29	37	100.0	184106	12	AC144662	AC144662 Rattus no
30	37	100.0	188181	5	AC073879	AC073879 Homo sapi
31	37	100.0	192769	11	BX571945	BX571945 Zebrafish
32	37	100.0	196040	12	EX936414	EX936414 Danio rer
33	37	100.0	198138	6	AC108443	AC108443 Mus muscu
34	37	100.0	198392	11	CR383678	CR383678 Zebrafish
35	37	100.0	198694	6	EX072557	EX072557 Mouse DNA
36	37	100.0	203905	12	AC166470	AC166470 Bos tauru
37	37	100.0	205476	12	AC139733	AC139733 Sus scrof
38	37	100.0	211542	6	AC126275	AC126275 Mus muscu
39	37	100.0	212186	6	AC132237	AC132237 Mus muscu
40	37	100.0	212556	6	AC127294	AC127294 Mus muscu
41	37	100.0	215694	12	AC162334	AC162334 Bos tauru
42	37	100.0	216921	12	BX322658	BX322658 Mus muscu
43	37	100.0	218094	12	AC094408	AC094408 Rattus no
44	37	100.0	219298	6	AC161378	AC161378 Mus muscu
45	37	100.0	227489	12	AC117015	AC117015 Rattus no
46	37	100.0	229617	12	AC110849	AC110849 Rattus no
47	37	100.0	231580	12	AC136817	AC136817 Rattus no
48	37	100.0	232346	6	CR974489	CR974489 Mouse DNA
49	37	100.0	235024	12	AC120681	AC120681 Rattus no
50	37	100.0	235183	12	AC079427	AC079427 Mus muscu
51	37	100.0	236235	12	AC120331	AC120331 Rattus no
52	37	100.0	239915	6	AC124977	AC124977 Mus muscu
53	37	100.0	240181	12	AC098105	AC098105 Rattus no
54	37	100.0	241481	12	AC160175	AC160175 Bos tauru
55	37	100.0	245996	12	AC096933	AC096933 Rattus no
56	37	100.0	259204	12	AC095370	AC095370 Rattus no
57	37	100.0	271699	12	AC095812	AC095812 Rattus no
58	37	100.0	282933	12	AC122970	AC122970 Rattus no
59	37	100.0	295904	12	AC119509	AC119509 Rattus no
60	35	94.6	2018	4	BT013437	BT013437 Lycopersi
61	35	94.6	2180	15	AY206432	AY206432 Shigella
62	35	94.6	16098	2	AX680082	AX680082 Sequence
63	35	94.6	37026	5	CNS00YVF	AL096808 Homo sapi
64	35	94.6	55700	5	AL583824	AL583824 Human DNA
65	35	94.6	107000	5	AC069417	AC069417 Homo sapi
66	35	94.6	118402	12	AC182438	AC182438 Zea mays
67	35	94.6	126697	15	CP000037	CP000037 Shigella
68	35	94.6	131716	12	AC025833	AC025833 Homo sapi
69	35	94.6	136694	15	AY879342	AY879342 Shigella
70	35	94.6	137248	6	AC124678	AC124678 Mus muscu
71	35	94.6	140306	5	HG1068F16	AL023913 Human DNA
72	35	94.6	142152	12	AC139658	AC139658 Rattus no
73	35	94.6	147700	12	AC162733	AC162733 Loxodonta
74	35	94.6	154684	5	AC093763	AC093763 Homo sapi
75	35	94.6	165216	12	AC079092	AC079092 Homo sapi
76	35	94.6	166238	12	AC019280	AC019280 Homo sapi

77	35	94.6	168700	12	AC009115	AC009115 Homo sapi	C 150	34	91.9	145796	4	AC130598	AC130598 Oryza sat
78	35	94.6	173911	5	AL354992	AL354992 Human DNA	C 151	34	91.9	146492	4	AC136223	AC136223 Oryza sat
79	35	94.6	177738	5	AC021593	AC021593 Homo sapi	C 152	34	91.9	146958	12	CT573437	CT573437 Pan trogl
80	35	94.6	182726	15	CP000035	CP000035 Shigella	C 153	34	91.9	148720	12	BX327319	BX327319 Mus muscu
81	35	94.6	185321	12	AC173169	AC173169 Bos tauru	C 154	34	91.9	151772	6	AC109294	AC109294 Mus muscu
82	35	94.6	190171	12	AC149270	AC149270 Zea mays	C 155	34	91.9	151863	12	AC179790	AC179790 Strongylo
83	35	94.6	201661	12	AC171488	AC171488 Bos tauru	C 156	34	91.9	152476	12	AP001869	AP001869 Homo sapi
84	35	94.6	202678	12	AC135648	AC135648 Rattus no	C 157	34	91.9	152951	5	AC026371	AC026371 Homo sapi
85	35	94.6	213494	15	SPWR100	SPWR100 Shigella	C 158	34	91.9	153178	12	AC009929	AC009929 Homo sapi
86	35	94.6	214396	15	CP000039	CP000039 Shigella	C 159	34	91.9	153713	6	AC119889	AC119889 Mus muscu
87	35	94.6	218596	11	CR751234	CR751234 Zebrafish	C 160	34	91.9	154959	6	AL662881	AL662881 Mouse DNA
88	35	94.6	221493	12	AC098143	AC098143 Rattus no	C 161	34	91.9	155410	12	AC179303	AC179303 Strongylo
89	35	94.6	221618	15	AF386526	AF386526 Shigella	C 162	34	91.9	155451	12	AC067774	AC067774 Homo sapi
90	35	94.6	221851	15	AF348706	AF348706 Shigella	C 163	34	91.9	155547	6	AC132595	AC132595 Mus muscu
91	35	94.6	225039	12	AC111941	AC111941 Rattus no	C 164	34	91.9	155691	12	AC023214	AC023214 Homo sapi
92	35	94.6	226546	6	AL807234	AL807234 Mouse DNA	C 165	34	91.9	156500	12	CR792441	CR792441 Danio rer
93	35	94.6	235671	12	AC130022	AC130022 Rattus no	C 166	34	91.9	157652	5	AC135851	AC135851 Homo sapi
94	35	94.6	236372	12	AC098033	AC098033 Rattus no	C 167	34	91.9	158039	6	AL663110	AL663110 Mouse DNA
95	35	94.6	238075	12	AC127907	AC127907 Rattus no	C 168	34	91.9	160799	12	AC177126	AC177126 Strongylo
96	35	94.6	257222	12	AC108271	AC108271 Rattus no	C 169	34	91.9	161154	6	AC116868	AC116868 Mus muscu
97	35	94.6	263390	12	AC172070	AC172070 Bos tauru	C 170	34	91.9	164715	12	AC161706	AC161706 Orolemur
98	35	94.6	264661	12	AC103215	AC103215 Rattus no	C 171	34	91.9	166166	5	AC079380	AC079380 Homo sapi
99	34	91.9	376	2	CQ441235	CQ441235 Sequence	C 172	34	91.9	166930	11	AC146690	AC146690 Gaeterost
100	34	91.9	410	4	AB016143	AB016143 Solanum m	C 173	34	91.9	166976	12	AC034274	AC034274 Homo sapi
101	34	91.9	622	7	BV354507	BV354507 S231P686R	C 174	34	91.9	167589	12	AC034274	AC034274 Strongylo
102	34	91.9	1981	2	AR671031	AR671031 Sequence	C 175	34	91.9	168025	12	AC024364	AC024364 Homo sapi
103	34	91.9	1981	5	AK056166	AK056166 Homo sapi	C 176	34	91.9	168197	6	AC137511	AC137511 Mus muscu
104	34	91.9	2000	2	AX509675	AX509675 Sequence	C 177	34	91.9	168293	12	AC018397	AC018397 Homo sapi
105	34	91.9	2000	2	AX652380	AX652380 Sequence	C 178	34	91.9	168443	12	AC137940	AC137940 Mus muscu
106	34	91.9	2229	7	BV178520	BV178520 sqm10107	C 179	34	91.9	169243	5	AC104816	AC104816 Homo sapi
107	34	91.9	2422	5	BC063873	BC063873 Homo sapi	C 180	34	91.9	169310	6	AC119259	AC119259 Mus muscu
108	34	91.9	2448	2	AX684874	AX684874 Sequence	C 181	34	91.9	171790	6	BX537331	BX537331 Mouse DNA
109	34	91.9	2959	5	AK092222	AK092222 Homo sapi	C 182	34	91.9	172476	5	AC007736	AC007736 Homo sapi
110	34	91.9	3221	11	BC084750	BC084750 Xenopus 1	C 183	34	91.9	172507	5	AC092960	AC092960 Homo sapi
111	34	91.9	3740	4	USMT01	L320171 Ustilago ma	C 184	34	91.9	172549	12	AC027519	AC027519 Homo sapi
112	34	91.9	3951	4	AX099660	AX099660 Arabidops	C 185	34	91.9	172613	5	AC113398	AC113398 Homo sapi
113	34	91.9	5379	2	AX345232	AX345232 Arabidops	C 186	34	91.9	174923	12	AC023350	AC023350 Homo sapi
114	34	91.9	14096	15	AF084104	AF084104 Bacillus	C 187	34	91.9	175419	12	AC177128	AC177128 Strongylo
115	34	91.9	16293	15	AC003950	AC003950 Xylella f	C 188	34	91.9	175737	12	AC147487	AC147487 Orolemur
116	34	91.9	18120	4	NCOA	XI4603 Neurospora	C 189	34	91.9	176692	12	AC164601	AC164601 Mus muscu
117	34	91.9	18215	13	U97552	U97552 Caenorhabdi	C 190	34	91.9	177771	6	AC115949	AC115949 Mus muscu
118	34	91.9	36020	13	CEC12D8	CEC12D8 Caenorhabdi	C 191	34	91.9	178011	6	AC129572	AC129572 Mus muscu
119	34	91.9	45962	12	AC006498	AC006498 Neurospor	C 192	34	91.9	179888	6	AC102287	AC102287 Mus muscu
120	34	91.9	52089	12	CR352281	CR352281 Homo sapi	C 193	34	91.9	179968	12	AC140813	AC140813 Homo sapi
121	34	91.9	57073	15	BA000038_18	Continuation (19 o	C 194	34	91.9	180001	5	AC112196	AC112196 Homo sapi
122	34	91.9	59652	12	AC137082	AC137082 Danio rer	C 195	34	91.9	181585	12	AC128628	AC128628 Rattus no
123	34	91.9	69126	5	AL354752	AL354752 Human DNA	C 196	34	91.9	181589	11	AC146544	AC146544 Gaeterost
124	34	91.9	84432	4	AC005850	AC005850 Human DNA	C 197	34	91.9	183218	6	AC132440	AC132440 Mus muscu
125	34	91.9	85745	11	BX936340	BX936340 Zebrafish	C 198	34	91.9	183544	6	AC102132	AC102132 Strongylo
126	34	91.9	85745	12	AC136769	AC136769 Homo sapi	C 199	34	91.9	189246	12	AC177713	AC177713 Strongylo
127	34	91.9	85745	12	AP008104	AP008104 Lotus cor	C 200	34	91.9	189263	12	AC176030	AC176030 Strongylo
128	34	91.9	95954	12	AC177384	AC177384 Strongylo	C 201	34	91.9	190504	12	AC172352	AC172352 Bos tauru
129	34	91.9	95972	12	AL353639	AL353639 Human DNA	C 202	34	91.9	190840	6	AC165968	AC165968 Mus muscu
130	34	91.9	103822	5	AL353639	AL353639 Mouse DNA	C 203	34	91.9	191494	6	AL591488	AL591488 Mouse DNA
131	34	91.9	108176	6	AL845327	Continuation (2 of	C 204	34	91.9	191946	12	AC177237	AC177237 Strongylo
132	34	91.9	110000	4	CR382126_01	Continuation (17 o	C 205	34	91.9	192636	12	AC174858	AC174858 Callicebu
133	34	91.9	110000	4	AP008211_016	Continuation (82 o	C 206	34	91.9	193489	6	AC158347	AC158347 Mus muscu
134	34	91.9	110000	4	AP008211_081	Continuation (39 o	C 207	34	91.9	193765	12	AC118517	AC118517 Rattus no
135	34	91.9	110000	15	AE015451_38	Continuation (13 o	C 208	34	91.9	193857	12	AC109541	AC109541 Rattus no
136	34	91.9	110000	15	AE016796_12	Continuation (18 o	C 209	34	91.9	194156	12	AC182058	AC182058 Bos tauru
137	34	91.9	110000	15	BA000038_17	Continuation (17 o	C 210	34	91.9	195733	6	AL928960	AL928960 Mouse DNA
138	34	91.9	118955	5	AC068274	AC068274 Homo sapi	C 211	34	91.9	196152	5	AC021242	AC021242 Homo sapi
139	34	91.9	124074	5	HS112520	BS222557 Homo sapi	C 212	34	91.9	196567	12	AC178103	AC178103 Strongylo
140	34	91.9	128898	12	AC147464	AC147464 Orolemur	C 213	34	91.9	196916	6	AC164402	AC164402 Mus muscu
141	34	91.9	133202	5	AL139182	AL139182 Human DNA	C 214	34	91.9	197879	11	AC146543	AC146543 Gaeterost
142	34	91.9	134928	12	AC168497	AC168497 Strongylo	C 215	34	91.9	197906	6	AC153422	AC153422 Mus muscu
143	34	91.9	135301	12	AC175999	AC175999 Strongylo	C 216	34	91.9	200910	6	AC083946	AC083946 Mus muscu
144	34	91.9	137285	12	AC113357	AC113357 Homo sapi	C 217	34	91.9	201282	6	AC132450	AC132450 Mus muscu
145	34	91.9	137690	12	AC151647	AC151647 Dasyypus n	C 218	34	91.9	201625	12	AC012144	AC012144 Homo sapi
146	34	91.9	138302	5	AC108060	AC108060 Homo sapi	C 219	34	91.9	202686	11	AC146539	AC146539 Gaeterost
147	34	91.9	139977	12	CR456630	CR456630 Danio rer	C 220	34	91.9	203246	12	AC162046	AC162046 Bos tauru
148	34	91.9	142740	6	AC103674	AC103674 Mus muscu	C 221	34	91.9	203422	6	AL713863	AL713863 Mouse DNA
149	34	91.9	143111	12	CR626923	CR626923 Danio rer	C 222	34	91.9	204899	5	AC117457	AC117457 Homo sapi

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 12, 2006, 21:08:36 ; Search time 3103 Seconds

(without alignments)
189.221 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 7

Sequence: 1 YLTQPS 7

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 48236798 seqs, 27959665780 residues

Word size: 1

Total number of hits satisfying chosen parameters: 96457779

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:

-MODEL=frame+*_p2n.model -DEV=xlh
-Q=/abs/ABSSWB-epool/US10537648/runat_12102006_151454_15415/app_query.fasta.1
-DB=EST -QFMT=fastap -SUFFIX=p2n.olig.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=1000
-DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=100 -MODE=LOCAL -OUTFMT=ptc
-NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs02h
-USER=US10537648-CCGN_1_6323-@runat_12102006_151454_15415 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOPT=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database :

EST: *
1: gb_est1: *
2: gb_est3: *
3: gb_est4: *
4: gb_est5: *
5: gb_est6: *
6: gb_est7: *
7: gb_est8: *
8: gb_est9: *
9: gb_est10: *
10: gb_est11: *
11: gb_est12: *
12: gb_est13: *
13: gb_est14: *
14: gb_est15: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	288	7	BB358863
2	7	100.0	304	6	AK200728
3	7	100.0	320	12	CE853641
4	7	100.0	331	11	A2240574

5	7	100.0	346	9	DA534392
6	7	100.0	392	13	CZ638826
7	7	100.0	413	11	AQ252207
8	7	100.0	458	14	DE130155
9	7	100.0	475	14	CR176637
10	7	100.0	494	14	CR192824
11	7	100.0	509	11	AQ464802
12	7	100.0	511	14	CR260251
13	7	100.0	515	14	CR251702
14	7	100.0	571	2	BZ838064
15	7	100.0	620	12	BZ879825
16	7	100.0	633	2	BZ826782
17	7	100.0	692	12	BZ921378
18	7	100.0	726	11	AQ077211
19	7	100.0	743	2	BZ830318
20	7	100.0	755	14	CR149426
21	7	100.0	769	14	AG494285
22	7	100.0	790	11	BH598970
23	7	100.0	797	14	BX966213
24	7	100.0	798	14	CR130680
25	7	100.0	801	14	BT047189
26	7	100.0	809	11	BH064279
27	7	100.0	815	13	CL831140
28	7	100.0	826	12	CG674428
29	7	100.0	826	14	AG866816
30	7	100.0	854	12	CC541008
31	7	100.0	859	12	CG818959
32	7	100.0	870	14	AG896133
33	7	100.0	987	14	CNS047BX
34	6	85.7	87	12	CG490574
35	6	85.7	100	8	CK211855
36	6	85.7	120	3	BM725400
37	6	85.7	125	3	BM677827
38	6	85.7	126	8	CN457244
39	6	85.7	134	7	BF440592
40	6	85.7	136	10	DV839525
41	6	85.7	144	2	BG463666
42	6	85.7	149	5	CK452301
43	6	85.7	149	5	CK453358
44	6	85.7	149	5	CK463686
45	6	85.7	149	5	CK464041
46	6	85.7	149	7	AW103591
47	6	85.7	149	9	DN120722
48	6	85.7	149	9	DN121075
49	6	85.7	150	13	CL631860
50	6	85.7	152	12	CE424767
51	6	85.7	162	3	BU034130
52	6	85.7	170	11	AZ218234
53	6	85.7	175	10	DM167722
54	6	85.7	178	7	BF395118
55	6	85.7	178	11	BH059583
56	6	85.7	181	2	BF922055
57	6	85.7	182	7	AW772133
58	6	85.7	186	1	AI300247
59	6	85.7	188	2	BM194624
60	6	85.7	194	12	BZ784599
61	6	85.7	195	1	AI283482
62	6	85.7	195	7	BB584501
63	6	85.7	198	1	AI381735
64	6	85.7	199	1	AJ705322
65	6	85.7	199	4	BY418866
66	6	85.7	201	1	AL376300
67	6	85.7	205	1	AI349368
68	6	85.7	212	5	CF107239
69	6	85.7	212	10	DY161690
70	6	85.7	214	1	AA977165
71	6	85.7	214	2	BG223350
72	6	85.7	216	11	BH490823
73	6	85.7	219	1	AI675377
74	6	85.7	219	1	AI970690
75	6	85.7	219	11	BH100187
76	6	85.7	221	1	AA105635
77	6	85.7	222	1	AA980984

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DE130155	Oryzias_1
CR176637	Reverse s
CR192824	Reverse s
AQ464802	HS_5105_B
CR260251	Reverse s
CR251702	Reverse s
BZ838064	BJ838064
BZ879825	CH240_293
BZ921378	CH240_119
AQ077211	CIT-HSP-2
BZ830318	BJ830318
CR149426	Reverse s
AG494285	Mus muscu
BH598970	BGGVellTF
BX966213	Reverse s
CR130680	Reverse s
BT047189	Sus scrofa
BH064279	RPCI-24-3
CL831140	OR_CBA005
CG674428	Trs2160 c
AG866816	Oryza sat
CC541008	CH240_421
CG818959	SOYCD72TH
AG896133	Oryza sat
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CG490574	OST27777
CK211855	MNS15676
BM725400	UI-E-EJO-
BM677827	UI-E-EJO-
CN457244	UI-M-HPO-
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DV839525	LB01125.C
BG463666	EMI_50_E0
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CK453358	909061 MA
CK463686	934608 MA
CK464041	934992 MA
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DN120722	1120763 M
DN121075	1121147 M
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CE424767	tigr-gss-
BU034130	QHU3D02.y
AZ218234	Sheared D
DM167722	CLVY612.b
BF395118	UI-R-CMO-
BH059583	RPCI-24-9
BF922055	CM2-NT017
AW772133	hm67h08.x
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BM194624	TCAAP3Q13
BZ784599	PUGC282TD
AI283482	gh94c06.x
BB584501	BB584501
AI381735	te42e08.x
AJ705322	AJ705322
BY418866	BY418866
AL376300	MtBB22F10
AI349368	qp71a11.x
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DY161690	000703BEM
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BG223350	na179h05
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C 78	222	14	DU486164	DU486164	109842109	C 151	6	85.7	310	10	DM164859
C 79	225	2	BI003642	PMO-HN007		152	6	85.7	313	9	D80302
C 80	227	2	BI297998	UI-R-CV2-		153	6	85.7	313	13	CW511846
C 81	227	7	BF230266	251788 BA		154	6	85.7	314	5	CD856816
C 82	228	1	AI254348	qu5c05.x		155	6	85.7	314	8	CN223696
C 83	228	1	AI254348	qu5c05.x		156	6	85.7	316	8	CR740891
C 84	229	1	AV323627	AV323627		157	6	85.7	318	7	BE252401
C 85	231	7	BA78527	BA78527		158	6	85.7	318	11	BA491696
C 86	232	8	CR519429	CR519429		159	6	85.7	321	5	CD858065
C 87	236	4	EX831501	EX831501		160	6	85.7	321	10	R02114
C 88	236	7	AW815701	AW815701		161	6	85.7	322	2	EG228330
C 89	237	1	AI280359	AI280359		162	6	85.7	322	13	CL706266
C 90	238	1	AA014107	AA014107		163	6	85.7	324	2	EG210367
C 91	238	1	AI370845	AI370845		164	6	85.7	324	10	DY244238
C 92	241	5	CK261554	CK261554		165	6	85.7	335	13	CW511508
C 93	244	2	EG588726	EG588726		166	6	85.7	337	1	AA118077
C 94	247	11	AZ464767	AZ464767		167	6	85.7	337	13	CL631399
C 95	250	1	AV292176	AV292176		168	6	85.7	339	3	BM934523
C 96	251	3	BQ007023	BQ007023		169	6	85.7	339	5	CD857729
C 97	252	1	AI934697	AI934697		170	6	85.7	339	10	F11225
C 98	252	7	AW663956	AW663956		171	6	85.7	339	11	AZ462826
C 99	252	7	BE950873	BE950873		172	6	85.7	331	7	BE532596
C 100	253	9	D801176	D801176		173	6	85.7	333	7	AW125571
C 101	254	8	CR462247	CR462247		174	6	85.7	333	7	BE955670
C 102	254	9	D80313	D80313		175	6	85.7	333	12	CG485974
C 103	255	2	EG374398	EG374398		176	6	85.7	335	14	CR294455
C 104	255	2	EG811010	EG811010		177	6	85.7	336	2	BI028828
C 105	256	10	DW123126	DW123126		178	6	85.7	336	3	BO988183
C 106	257	7	BF447024	BF447024		179	6	85.7	338	1	AI414371
C 107	258	10	DV414893	DV414893		180	6	85.7	338	1	AU022166
C 108	262	2	BI297375	BI297375		181	6	85.7	338	11	CG577791
C 109	262	2	BI300146	BI300146		182	6	85.7	339	12	CG577791
C 110	263	7	BA339867	BA339867		183	6	85.7	340	1	AI237331
C 111	264	7	BA214710	BA214710		184	6	85.7	340	7	AW814070
C 112	268	10	DV771843	DV771843		185	6	85.7	340	9	CX562950
C 113	268	12	CE338107	CE338107		186	6	85.7	340	10	DY052161
C 114	270	12	CG487381	CG487381		187	6	85.7	341	4	BY111013
C 115	271	4	CA428913	CA428913		188	6	85.7	342	2	BF866333
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C 118	279	1	AA679398	AA679398		191	6	85.7	344	1	AA469244
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C 120	279	7	AW485727	AW485727		193	6	85.7	345	7	BB314189
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C 123	285	1	AA468535	AA468535		196	6	85.7	349	7	BB314013
C 124	285	11	AQ387436	AQ387436		197	6	85.7	350	1	AA030161
C 125	286	8	CO873481	CO873481		198	6	85.7	350	12	CG493272
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C 127	288	2	EG204927	EG204927		200	6	85.7	353	7	AW008907
C 128	288	3	EG648917	EG648917		201	6	85.7	353	12	CE707150
C 129	288	4	EX303555	EX303555		202	6	85.7	353	8	CK977658
C 130	289	1	AI711077	AI711077		203	6	85.7	356	7	AV775301
C 131	289	3	BM510733	BM510733		204	6	85.7	357	9	DA719661
C 132	290	4	CD077602	CD077602		205	6	85.7	359	1	AA647386
C 133	290	5	CD705379	CD705379		206	6	85.7	359	1	AA726908
C 134	290	11	B37454	B37454		207	6	85.7	362	12	CG564561
C 135	291	7	BF560952	BF560952		208	6	85.7	363	7	BO584567
C 136	294	1	AA291494	AA291494		209	6	85.7	363	7	BB805097
C 137	294	10	DY152116	DY152116		210	6	85.7	363	12	CE760902
C 138	295	1	AA907539	AA907539		211	6	85.7	365	3	BU522899
C 139	295	1	AV141194	AV141194		212	6	85.7	365	11	AZ482660
C 140	295	8	CR461685	CR461685		213	6	85.7	366	12	CG483920
C 141	296	1	AV086855	AV086855		214	6	85.7	366	13	CL610380
C 142	297	2	EG730052	EG730052		215	6	85.7	367	2	EG088127
C 143	298	7	BA458994	BA458994		216	6	85.7	367	14	CR148713
C 144	299	1	AA473686	AA473686		217	6	85.7	368	10	DY042483
C 145	301	11	AQ632796	AQ632796		218	6	85.7	369	13	CL569078
C 146	305	8	CO886548	CO886548		219	6	85.7	370	3	BP386340
C 147	306	12	CG561977	CG561977		220	6	85.7	370	12	CG513120
C 148	308	1	AU150143	AU150143		221	6	85.7	371	2	BU959532
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DM164859 CLVY3403.
 D80302 HUM059H11B
 CW511846 Shotgun G
 CD856816 DHOAG242A
 CN223696 WLA05IA04
 CR740891 CR740891
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 CD858065 DHOAG82A0
 R02114 ye83e06.e1
 EG228330 uxl1f12.x
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 CL569078 CMHD-GT_1
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 BU959532 BU959532
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 AI216186 qm41g10.x

GenCore version 5.1.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 12, 2006, 21:37:51 ; Search time 852 Seconds

(without alignments)

151.432 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 7

Sequence: 1 YLTPQS 7

Scoring table:
OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 18892170 seqs, 614381738 residues

Word size: 1

Total number of hits satisfying chosen parameters: 37649232

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters: -DEV=xlh

-Q=/abss/ABSSWEB_spool/US10537648/runat_12102006_151504_15561/app_query.fasta_1
-DB=Published Applications NA Main -QFMT=fastap -SUFFIX=p2n.olig.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=1000 -DOCALLIGN=200 -THR SCORE=quality -THR MIN=1
-ALIGN=100 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-NO MMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
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Database : Published Applications NA Main:*

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12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
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14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	6	85.7	21	11	US-10-310-914A-581754 Sequence 581754,

C 2	6	85.7	22	11	US-10-310-914A-1212172 Sequence 1212172,
C 3	6	85.7	24	11	US-10-310-914A-581792 Sequence 581792,
C 4	6	85.7	25	9	US-10-719-900-702816 Sequence 702816,
5	6	85.7	25	11	US-10-932-182A-181503 Sequence 181503,
6	6	85.7	180	9	US-10-674-124A-4967 Sequence 4967, Ap
7	6	85.7	201	9	US-10-719-993-4501 Sequence 4501, Ap
8	6	85.7	201	9	US-10-719-993-4507 Sequence 4507, Ap
C 9	6	85.7	201	9	US-10-719-993-4528 Sequence 4528, Ap
C 10	6	85.7	201	9	US-10-719-993-4534 Sequence 4534, Ap
C 11	6	85.7	201	9	US-10-719-993-4557 Sequence 4557, Ap
C 12	6	85.7	201	9	US-10-719-993-4563 Sequence 4563, Ap
C 13	6	85.7	201	9	US-10-719-993-4587 Sequence 4587, Ap
C 14	6	85.7	201	9	US-10-719-993-4592 Sequence 4592, Ap
C 15	6	85.7	201	9	US-10-719-993-4614 Sequence 4614, Ap
C 16	6	85.7	201	9	US-10-719-993-4620 Sequence 4620, Ap
17	6	85.7	201	9	US-10-741-600-26779 Sequence 26779, A
C 18	6	85.7	201	16	US-11-124-367A-2491 Sequence 2491, Ap
C 19	6	85.7	201	16	US-11-124-367A-2497 Sequence 2497, Ap
C 20	6	85.7	201	16	US-11-124-367A-2522 Sequence 2522, Ap
C 21	6	85.7	201	16	US-11-124-367A-2526 Sequence 2526, Ap
C 22	6	85.7	201	16	US-11-124-367A-2537 Sequence 2537, Ap
C 23	6	85.7	201	16	US-11-124-367A-2543 Sequence 2543, Ap
C 24	6	85.7	201	16	US-11-124-367A-2566 Sequence 2566, Ap
C 25	6	85.7	201	16	US-11-124-367A-2570 Sequence 2570, Ap
C 26	6	85.7	201	16	US-11-124-367A-2583 Sequence 2583, Ap
C 27	6	85.7	201	16	US-11-124-367A-2588 Sequence 2588, Ap
C 28	6	85.7	201	16	US-11-124-367A-2612 Sequence 2612, Ap
C 29	6	85.7	201	16	US-11-124-367A-2615 Sequence 2615, Ap
C 30	6	85.7	201	16	US-11-124-367A-2626 Sequence 2626, Ap
C 31	6	85.7	201	16	US-11-124-367A-2632 Sequence 2632, Ap
C 32	6	85.7	201	16	US-11-124-367A-2656 Sequence 2656, Ap
C 33	6	85.7	201	16	US-11-124-367A-2660 Sequence 2660, Ap
C 34	6	85.7	201	16	US-11-124-367A-2672 Sequence 2672, Ap
C 35	6	85.7	201	16	US-11-124-367A-2674 Sequence 2674, Ap
C 36	6	85.7	201	16	US-11-124-367A-2698 Sequence 2698, Ap
C 37	6	85.7	201	16	US-11-124-367A-2698 Sequence 2698, Ap
38	6	85.7	251	9	US-10-425-115-166919 Sequence 166919,
39	6	85.7	292	3	US-09-867-701-2840 Sequence 2840, A
C 40	6	85.7	294	3	US-09-867-701-2840 Sequence 2840, A
C 41	6	85.7	305	8	US-10-424-599-59154 Sequence 59154, A
C 42	6	85.7	323	9	US-10-425-115-106513 Sequence 106513,
C 43	6	85.7	376	9	US-10-425-115-123375 Sequence 123375,
C 44	6	85.7	392	3	US-09-930-213-71 Sequence 71, Appl
C 45	6	85.7	434	9	US-10-425-115-39544 Sequence 39544, A
46	6	85.7	447	3	US-09-470-276-69 Sequence 69, Appl
47	6	85.7	447	8	US-10-680-386-69 Sequence 69, Appl
48	6	85.7	448	10	US-10-631-467-1243 Sequence 1243, Ap
C 49	6	85.7	469	3	US-09-864-761-15741 Sequence 15741, A
50	6	85.7	497	12	US-10-301-480-279612 Sequence 279612,
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C 52	6	85.7	501	4	US-09-925-065A-535602 Sequence 535602,
C 53	6	85.7	501	5	US-09-925-065A-535602 Sequence 535602,
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C 56	6	85.7	506	4	US-09-925-065A-760213 Sequence 760213,
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68	6	85.7	527	5	US-09-925-065A-331874 Sequence 331874,
69	6	85.7	530	4	US-09-925-065A-187047 Sequence 187047,
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C 71	6	85.7	539	4	US-09-925-065A-871889 Sequence 871889,
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C 73	6	85.7	539	5	US-09-925-065A-902648 Sequence 902648,
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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 12, 2006, 21:08:51 ; Search time 145 Seconds
(without alignments)
135.494 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 7

Sequence: 1 YLTQPS 7

Scoring table:

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Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 1403666 seqs, 935554401 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2786218

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	6	85.7	601	3 US-09-949-016-30525	Sequence 30525, A
5	6	85.7	601	3 US-09-949-016-37144	Sequence 37144, A
6	6	85.7	601	3 US-09-949-016-37158	Sequence 37158, A
C 7	6	85.7	601	3 US-09-949-016-44638	Sequence 44638, A

8	6	85.7	601	3	US-09-949-016-76098	Sequence 76098, A
9	6	85.7	601	3	US-09-949-016-103077	Sequence 103077, A
10	6	85.7	601	3	US-09-949-016-103152	Sequence 103152, A
C 11	6	85.7	601	3	US-09-949-016-115548	Sequence 115548, A
C 12	6	85.7	601	3	US-09-949-016-115641	Sequence 115641, A
C 13	6	85.7	601	3	US-09-949-016-115734	Sequence 115734, A
C 14	6	85.7	601	3	US-09-949-016-115827	Sequence 115827, A
C 15	6	85.7	601	3	US-09-949-016-115920	Sequence 115920, A
C 16	6	85.7	601	3	US-09-949-016-116013	Sequence 116013, A
C 17	6	85.7	601	3	US-09-949-016-116106	Sequence 116106, A
C 18	6	85.7	601	3	US-09-949-016-116199	Sequence 116199, A
C 19	6	85.7	601	3	US-09-949-016-116292	Sequence 116292, A
C 20	6	85.7	601	3	US-09-949-016-116385	Sequence 116385, A
C 21	6	85.7	601	3	US-09-949-016-145862	Sequence 145862, A
C 22	6	85.7	601	3	US-09-949-016-146130	Sequence 146130, A
C 23	6	85.7	601	3	US-09-949-016-146398	Sequence 146398, A
C 24	6	85.7	601	3	US-09-949-016-148718	Sequence 148718, A
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C 30	6	85.7	601	3	US-09-949-016-186632	Sequence 186632, A
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C 34	6	85.7	1116	3	US-09-543-681A-739	Sequence 739, App
C 35	6	85.7	1128	3	US-09-543-681A-41	Sequence 41, Appl
C 36	6	85.7	1216	3	US-08-838-151A-62	Sequence 62, Appl
C 37	6	85.7	2812	3	US-09-620-312D-624	Sequence 624, Appl
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C 39	6	85.7	3999	3	US-09-286-891-1	Sequence 1, Appl
C 40	6	85.7	5345	2	US-08-044-618-7	Sequence 7, Appl
C 41	6	85.7	19152	3	US-09-949-016-12110	Sequence 12110, A
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C 43	6	85.7	19826	3	US-09-949-016-16973	Sequence 16973, A
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C 46	6	85.7	27150	3	US-09-593-828-20	Sequence 20, Appl
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C 57	6	85.7	52523	3	US-09-949-016-12433	Sequence 12433, A
C 58	6	85.7	52530	3	US-09-949-016-13948	Sequence 13948, A
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114	5	71.4	28	3	US-09-225-928-1084	Sequence 1084, Ap	187	5	71.4	330	3	FCT-US95-08596-1	Sequence 57, Appl
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124	5	71.4	35	2	US-09-374-671A-37	Sequence 37, Appl	c 197	5	71.4	372	3	US-09-513-999C-13009	Sequence 13009, A
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127	5	71.4	46	2	US-08-778-487-20	Sequence 20, Appl	c 200	5	71.4	388	3	US-09-513-999C-1746	Sequence 1746, Ap
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130	5	71.4	46	3	US-09-136-801-32	Sequence 32, Appl	c 203	5	71.4	396	3	US-09-713-550-47	Sequence 47, Appl
131	5	71.4	46	3	US-09-202-088A-32	Sequence 32, Appl	c 204	5	71.4	396	3	US-09-825-294-47	Sequence 47, Appl
132	5	71.4	50	3	US-10-131-827-772	Sequence 772, App	c 205	5	71.4	396	3	US-09-970-966-47	Sequence 47, Appl
133	5	71.4	50	3	US-10-131-831-772	Sequence 772, App	c 206	5	71.4	404	3	US-09-513-999C-28470	Sequence 28470, A
134	5	71.4	56	3	US-10-014-012-204	Sequence 204, App	c 207	5	71.4	406	3	US-09-195-106-10	Sequence 10, Appl
135	5	71.4	66	3	US-09-625-188-44	Sequence 44, Appl	208	5	71.4	416	3	US-08-945-140-5	Sequence 5, Appl
136	5	71.4	71	2	US-08-477-527A-43	Sequence 43, Appl	209	5	71.4	421	3	US-09-513-999C-27809	Sequence 27809, A
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145	5	71.4	79	3	US-09-834-759-304	Sequence 304, App	c 218	5	71.4	460	4	US-09-880-107-3518	Sequence 3518, Ap
146	5	71.4	79	3	US-09-590-751A-304	Sequence 304, App	c 219	5	71.4	462	3	US-09-499-522-6	Sequence 6, Appl
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148	5	71.4	79	3	US-09-551-621A-304	Sequence 304, App	221	5	71.4	466	3	US-09-409-938-7	Sequence 7, Appl
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150	5	71.4	79	4	US-10-124-805-304	Sequence 304, App	c 223	5	71.4	470	3	US-09-513-999C-9486	Sequence 9486, Ap
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Aac75508	Human ORF	6	6	AAC75508
Abn17552	Human ORF	285	3	ABN17552
Abx83523	Corn ear-	6	6	ABX83523
Abi179862	Human ova	289	10	ABI179862
Ado41272	Human cDN	6	6	ADO41272
Aah10981	Human cDN	308	4	AH10981
Adh40722	Rat cardi	6	6	ADH40722
Adb56138	Toxicity-	340	13	ADB56138
Adb50665	Primary r	347	10	ADB50665
Abn19259	Human ORF	347	10	ABN19259
Aah81562	Human dif	376	6	AH81562
Acf86753	Human SIR	392	5	ACF86753
Aah05178	Human MSH	411	13	AH05178
Adj75991	Marker ge	447	2	ADJ75991
Adu12670	Solid tum	448	12	ADU12670
Abso7083	Human gen	461	13	ABSO7083
Acf81501	Human SIR	469	6	ACF81501
Aah09146	Human cDN	492	13	AH09146
Aah81588	Human dif	517	4	AH81588
Acso1861	C. glutam	541	5	ACSO1861
Abae1762	Human foe	549	8	ABAE1762
Aai1679	Probe #10	574	4	AAI1679
Aak35966	Human bon	574	4	AAK35966
Aak10071	Human bra	574	4	AAK10071
Abso10166	Human liv	574	4	ABSO10166
Abso10166	Human gen	574	4	ABSO10166
Ado34573	Human SLI	576	12	ADO34573
Adk52858	Plant DNA	584	10	ADK52858
Aah65078	C glutam	660	5	AH65078
Aed72487	Corynebac	672	14	AED72487
Aah07063	Human cDN	681	4	AH07063
Aak64512	Human imm	719	4	AAK64512
Abq40170	Oligonuc	740	6	ABQ40170
Abq40171	Oligonuc	740	6	ABQ40171
Aaa01846	Human col	749	3	AAA01846
Adt41963	Bacterial	762	13	ADT41963
Adt29407	Rice abio	830	11	ADT29407
Abx78336	Soybean s	852	10	ABX78336
Aef94154	Stress re	852	15	AEF94154
Aah34154	Human col	866	4	AH34154
Aac59004	Human sec	870	3	AAC59004
Aaf08009	Fusarium	892	3	AAF08009
Adu52050	Fusarium	892	13	ADU52050
Adz90053	Fusarium	892	14	ADZ90053
Acas3447	Prokaryot	993	8	ACA3447
Abx78337	Soybean s	1041	10	ABX78337
Aef94156	Stress re	1041	15	AEF94156
Aee11565	Hamster c	1084	14	AEE11565
Ada70953	Rice gene	1116	8	ADA70953
Adf00454	Bacterial	1116	10	ADF00454
Ades9755	Bacterial	1116	10	ADE9755
Aat93320	Tomato-in	1216	2	AAT93320
Abk35925	cDNA sequ	1354	6	ABK35925
Aac64784	Lemon alc	1436	3	AAC64784
Abv87054	Human col	1452	6	ABV87054
Aal48581	A thalian	1539	6	AAL48581
Aah18582	Human cDN	1591	4	AH18582
Aaz96758	Nuclear t	1605	3	AZ96758
Aah1760	Human dif	1605	5	AH1760
Aed73304	Human pla	1734	14	AED73304
Acas4446	Prokaryot	1797	8	ACA4446
Ade59433	Human gen	1898	4	ADE59433
Aas45223	cDNA enco	1932	10	AAS45223
Abz16565	Arabidops	1943	5	ABZ16565
Ada68927	Arabidops	2000	6	ADA68927
Ada02929	Mouse Pik	2000	8	ADA02929
Adb72667	Mouse Pik	2175	9	ADB72667
Adc85409	Mouse Pik	2175	10	ADC85409
Adm74524	Murine ca	2175	12	ADM74524

77	6	85.7	2178	9	ADB08415	AdB08415	Alloiooc	150	6	85.7	16555	4	AAK70102	AAK70102 Human imm
78	6	85.7	2178	9	ADB08417	AdB08417	Alloiooc	151	6	85.7	19969	4	AAK65309	AAK65309 Human imm
79	6	85.7	2178	9	ADB08413	AdB08413	Alloiooc	152	6	85.7	20598	4	AAK65309	AAK65309 Human imm
80	6	85.7	2209	4	AAH17074	AAH17074	Human CDN	153	6	85.7	20598	4	AAK65309	AAK65309 Human imm
81	6	85.7	2209	13	ADO87393	AdO87393	Human CDN	154	6	85.7	20598	4	AAK65309	AAK65309 Human imm
82	6	85.7	2215	4	AAH15419	AAH15419	Human CDN	155	6	85.7	23885	4	AAK73173	AAK73173 Human imm
83	6	85.7	2232	6	ABK35916	ABK35916	CDNA sequ	156	6	85.7	23885	4	AAK73173	AAK73173 Human imm
84	6	85.7	2383	4	AAI93833	AAI93833	Human pol	157	6	85.7	24993	4	AAK70103	AAK70103 Human imm
85	6	85.7	2566	4	AAH17667	AAH17667	Human CDN	158	6	85.7	25373	12	ADK16022	ADK16022 Human imm
86	6	85.7	2569	10	ADC30261	AdC30261	Human nov	159	6	85.7	27150	4	AAK65726	AAK65726 Human imm
87	6	85.7	2607	12	ADO67217	AdO67217	Novel hum	160	6	85.7	27150	4	AAK65726	AAK65726 Human imm
88	6	85.7	2659	9	ABT43745	ABT43745	Molecule	161	6	85.7	27976	4	AAK70187	AAK70187 Human imm
89	6	85.7	2812	4	AAI58734	AAI58734	Human pol	162	6	85.7	27976	4	AAK70187	AAK70187 Human imm
90	6	85.7	2812	4	AAI60520	AAI60520	Human pol	163	6	85.7	32185	11	ACN44604	ACN44604 Mouse gen
91	6	85.7	2812	5	ADO98954	AdO98954	DNA encod	164	6	85.7	32185	11	ACN44604	ACN44604 Mouse gen
92	6	85.7	2812	9	ADB48714	AdB48714	Novel hum	165	6	85.7	32189	5	AAK30115	AAK30115 Human lun
93	6	85.7	2819	6	ABA93732	ABa93732	Human dif	166	6	85.7	32221	5	AAK30115	AAK30115 Human lun
94	6	85.7	2830	6	ABL58960	ABl58960	Human CDN	167	6	85.7	32221	5	AAK30115	AAK30115 Human lun
95	6	85.7	2830	12	ADL26751	AdL26751	Human SE2	168	6	85.7	32221	5	AAK30115	AAK30115 Human lun
96	6	85.7	2867	6	ABN84190	ABn84190	Human cel	169	6	85.7	32221	5	AAK30115	AAK30115 Human lun
97	6	85.7	2867	14	ADM14872	AdM14872	Human cel	170	6	85.7	32221	5	AAK30115	AAK30115 Human lun
98	6	85.7	2902	3	AAK46853	AAc46853	Arabidops	171	6	85.7	32221	5	AAK30115	AAK30115 Human lun
99	6	85.7	3256	5	ADL45276	AdL45276	Human ova	172	6	85.7	32221	5	AAK30115	AAK30115 Human lun
100	6	85.7	3256	5	ADL45276	AdL45276	Human ova	173	6	85.7	32221	5	AAK30115	AAK30115 Human lun
101	6	85.7	3289	8	ABX34745	ABx34745	Human mdd	174	6	85.7	32221	5	AAK30115	AAK30115 Human lun
102	6	85.7	3324	6	AAK594913	AAK594913	Human DNA	175	6	85.7	32221	5	AAK30115	AAK30115 Human lun
103	6	85.7	3339	13	ACN38144	ACn38144	Tumour-as	176	6	85.7	32221	5	AAK30115	AAK30115 Human lun
104	6	85.7	3452	12	ADM79346	AdM79346	Mouse lym	177	6	85.7	32221	5	AAK30115	AAK30115 Human lun
105	6	85.7	3454	6	ABK72319	ABk72319	Mouse F13	178	6	85.7	32221	5	AAK30115	AAK30115 Human lun
106	6	85.7	3454	6	ABK72319	ABk72319	DNA encod	179	6	85.7	32221	5	AAK30115	AAK30115 Human lun
107	6	85.7	3454	6	ABK72319	ABk72319	Lymphona	180	6	85.7	32221	5	AAK30115	AAK30115 Human lun
108	6	85.7	3454	6	ABK72319	ABk72319	Mouse CDN	181	6	85.7	32221	5	AAK30115	AAK30115 Human lun
109	6	85.7	3454	9	ABK72319	ABk72319	Mouse CDN	182	6	85.7	32221	5	AAK30115	AAK30115 Human lun
110	6	85.7	3454	10	ADB72666	AdB72666	Mouse Pik	183	6	85.7	32221	5	AAK30115	AAK30115 Human lun
111	6	85.7	3454	10	ADB72666	AdB72666	Mouse Pik	184	6	85.7	32221	5	AAK30115	AAK30115 Human lun
112	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	185	6	85.7	32221	5	AAK30115	AAK30115 Human lun
113	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	186	6	85.7	32221	5	AAK30115	AAK30115 Human lun
114	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	187	6	85.7	32221	5	AAK30115	AAK30115 Human lun
115	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	188	6	85.7	32221	5	AAK30115	AAK30115 Human lun
116	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	189	6	85.7	32221	5	AAK30115	AAK30115 Human lun
117	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	190	6	85.7	32221	5	AAK30115	AAK30115 Human lun
118	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	191	6	85.7	32221	5	AAK30115	AAK30115 Human lun
119	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	192	6	85.7	32221	5	AAK30115	AAK30115 Human lun
120	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	193	6	85.7	32221	5	AAK30115	AAK30115 Human lun
121	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	194	6	85.7	32221	5	AAK30115	AAK30115 Human lun
122	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	195	6	85.7	32221	5	AAK30115	AAK30115 Human lun
123	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	196	6	85.7	32221	5	AAK30115	AAK30115 Human lun
124	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	197	6	85.7	32221	5	AAK30115	AAK30115 Human lun
125	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	198	6	85.7	32221	5	AAK30115	AAK30115 Human lun
126	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	199	6	85.7	32221	5	AAK30115	AAK30115 Human lun
127	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	200	6	85.7	32221	5	AAK30115	AAK30115 Human lun
128	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	201	6	85.7	32221	5	AAK30115	AAK30115 Human lun
129	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	202	6	85.7	32221	5	AAK30115	AAK30115 Human lun
130	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	203	6	85.7	32221	5	AAK30115	AAK30115 Human lun
131	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	204	6	85.7	32221	5	AAK30115	AAK30115 Human lun
132	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	205	6	85.7	32221	5	AAK30115	AAK30115 Human lun
133	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	206	6	85.7	32221	5	AAK30115	AAK30115 Human lun
134	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	207	6	85.7	32221	5	AAK30115	AAK30115 Human lun
135	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	208	6	85.7	32221	5	AAK30115	AAK30115 Human lun
136	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	209	6	85.7	32221	5	AAK30115	AAK30115 Human lun
137	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	210	6	85.7	32221	5	AAK30115	AAK30115 Human lun
138	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	211	6	85.7	32221	5	AAK30115	AAK30115 Human lun
139	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	212	6	85.7	32221	5	AAK30115	AAK30115 Human lun
140	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	213	6	85.7	32221	5	AAK30115	AAK30115 Human lun
141	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	214	6	85.7	32221	5	AAK30115	AAK30115 Human lun
142	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	215	6	85.7	32221	5	AAK30115	AAK30115 Human lun
143	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	216	6	85.7	32221	5	AAK30115	AAK30115 Human lun
144	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	217	6	85.7	32221	5	AAK30115	AAK30115 Human lun
145	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	218	6	85.7	32221	5	AAK30115	AAK30115 Human lun
146	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	219	6	85.7	32221	5	AAK30115	AAK30115 Human lun
147	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	220	6	85.7	32221	5	AAK30115	AAK30115 Human lun
148	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	221	6	85.7	32221	5	AAK30115	AAK30115 Human lun
149	6	85.7	3454	12	ADM79373	AdM79373	Mouse lym	222	6	85.7	32221	5	AAK30115	AAK30115 Human lun

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 12, 2006, 21:02:56 ; Search time 3418 Seconds

(without alignments)

196.445 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 7

Sequence: 1 YLTQPS 7

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 6366136 seqs, 31973710525 residues

Word size: 1

Total number of hits satisfying chosen parameters: 12697109

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:
-MODEL=frame+ p2n model -DEV=xlh
-Q/abs/ABSWEB_spool/US10537648/runat_12102006_151451_15373/app_query.fasta_1
-DB=GenEmbl -OFT=fastap -SUFFIX=p2n.olig.rge -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNIT=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=1000 -DOALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=100 -MODE=LOCAL
-OUTFT=pcp -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs02h
-USER=US10537648 @CGN 1 1 5548 @runat_12102006_151451_15373 -NCPU=6 -ICPU=3
-NO_WMAP -NEG_SCORES=0 -WAIT -DSBLOK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database :

GenEmbl : *

1: gb_env:*

2: gb_pat:*

3: gb_ph:*

4: gb_pl:*

5: gb_pr:*

6: gb_ro:*

7: gb_sts:*

8: gb_sy:*

9: gb_un:*

10: gb_vi:*

11: gb_ov:*

12: gb_htg:*

13: gb_in:*

14: gb_om:*

15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	21	2	CQ828007 Sequence
2	7	100.0	2000	2	AX656858 Sequence
3	7	100.0	44681	13	AC092520 Ciona sav

4	7	100.0	69037	6	AC003949	AC003949 Mus muscu
5	7	100.0	92797	5	AF038458	AF038458 Homo sapi
6	7	100.0	99489	12	AC084843	AC084843 Homo sapi
7	7	100.0	103836	6	AC125670	AC125670 Rattus no
8	7	100.0	105538	4	OSJN00043	AL066612 Oryza sat
9	7	100.0	110000	4	AP008207_428	Continuation (429
10	7	100.0	110000	4	AP008210_007	Continuation (8 of
11	7	100.0	112833	12	AC153744	AC153744 Ornithorh
12	7	100.0	130225	12	AC177977	AC177977 Strongylo
13	7	100.0	131761	12	AC164507	AC164507 Loxodonta
14	7	100.0	135924	14	AC163264	AC163264 Rhinolph
15	7	100.0	137877	12	AC167095	AC167095 Sorex ara
16	7	100.0	139969	12	AC170718	AC170718 Atelerix
17	7	100.0	144819	12	AC173446	AC173446 Atelerix
18	7	100.0	148743	11	BX324154	BX324154 Zebrafish
19	7	100.0	151772	6	AC109294	AC109294 Mus muscu
20	7	100.0	155624	5	AC027058	AC027058 Homo sapi
21	7	100.0	165228	5	CNS01DMS	AL138479 Human chr
22	7	100.0	166758	12	AC173466	AC173466 Sorex ara
23	7	100.0	167388	12	AC157445	AC157445 Sus scrof
24	7	100.0	170875	6	AC154429	AC154429 Mus muscu
25	7	100.0	172427	5	AC161282	AC161282 Pan trogl
26	7	100.0	172853	5	AC084361	AC084361 Homo sapi
27	7	100.0	173555	4	AP003277	AP003277 Oryza sat
28	7	100.0	179085	5	AC175825	AC175825 Pan trogl
29	7	100.0	184106	12	AC144662	AC144662 Rattus no
30	7	100.0	188181	5	AC073879	AC073879 Homo sapi
31	7	100.0	192769	11	BX571945	BX571945 Zebrafish
32	7	100.0	196040	12	BX936414	BX936414 Danio rer
33	7	100.0	198138	6	AC108443	AC108443 Mus muscu
34	7	100.0	198392	11	CR383678	CR383678 Zebrafish
35	7	100.0	198694	6	BX072557	BX072557 Mouse DNA
36	7	100.0	203905	12	AC166470	AC166470 Bos tauru
37	7	100.0	205476	12	AC139733	AC139733 Sus scrof
38	7	100.0	211542	6	AC126275	AC126275 Mus muscu
39	7	100.0	212186	6	AC127294	AC127294 Mus muscu
40	7	100.0	215556	6	AC127294	AC127294 Mus muscu
41	7	100.0	215694	12	AC162334	AC162334 Bos tauru
42	7	100.0	216921	12	BX322658	BX322658 Mus muscu
43	7	100.0	218094	12	AC094408	AC094408 Rattus no
44	7	100.0	219298	6	AC161378	AC161378 Mus muscu
45	7	100.0	227489	12	AC117015	AC117015 Rattus no
46	7	100.0	229617	12	AC110849	AC110849 Rattus no
47	7	100.0	231580	12	AC136817	AC136817 Rattus no
48	7	100.0	232346	6	CR974489	CR974489 Mouse DNA
49	7	100.0	235024	12	AC120681	AC120681 Rattus no
50	7	100.0	235183	12	AC079427	AC079427 Mus muscu
51	7	100.0	236235	12	AC120331	AC120331 Rattus no
52	7	100.0	239915	6	AC124977	AC124977 Mus muscu
53	7	100.0	240181	12	AC098105	AC098105 Rattus no
54	7	100.0	241481	12	AC160175	AC160175 Bos tauru
55	7	100.0	246996	12	AC096933	AC096933 Rattus no
56	7	100.0	259204	12	AC095370	AC095370 Rattus no
57	7	100.0	271699	12	AC095812	AC095812 Rattus no
58	7	100.0	282933	12	AC122970	AC122970 Rattus no
59	7	100.0	295904	12	AC119509	AC119509 Rattus no
60	6	85.7	48	2	CQ654264	CQ654264 Sequence
61	6	85.7	170	7	G20553	G20553 human STS A
62	6	85.7	180	7	AB143874	AB143874 Homo sapi
63	6	85.7	202	7	G54653	G54653 AffySTS0000
64	6	85.7	202	7	G60148	G60148 SHGC-130789
65	6	85.7	227	7	HUMSTAF	M83622 Human satel
66	6	85.7	240	2	CQ820279	CQ820279 Sequence
67	6	85.7	240	10	AV303046	AV303046 Untyped h
68	6	85.7	250	5	AJ628945	AJ628945 Homo sapi
69	6	85.7	285	2	CQ437821	CQ437821 Sequence
70	6	85.7	289	2	AR246624	AR246624 Sequence
71	6	85.7	294	2	CQ460062	CQ460062 Sequence
72	6	85.7	296	15	AF536468	AF536468 Nocardia
73	6	85.7	298	15	AF536466	AF536466 Nocardia
74	6	85.7	308	2	BD152973	BD152973 Primer fo
75	6	85.7	308	2	AX872911	AX872911 Sequence
76	6	85.7	321	10	AF113567	AF113567 HIV-1 iso

C 77	6	85.7	326	5	HSRPS26D	X79236 Homo sapien	150	6	85.7	903	10	AB055923	AB055923 Human ech
C 78	6	85.7	334	7	BV244336	BV244336 S234P626F	151	6	85.7	903	10	AB055924	AB055924 Human ech
C 79	6	85.7	376	2	CQ441235	CQ441235 Sequence	C 152	6	85.7	927	15	AF261151	AF261151 Vibrio ch
C 80	6	85.7	391	7	G50827	G50827 SHGC-81169	153	6	85.7	1021	2	CQ731389	CQ731389 Sequence
C 81	6	85.7	391	11	PCMSAT6FR	Y12771 Phalacrocor	154	6	85.7	1038	4	AF490530	AF490530 Lycopersi
C 82	6	85.7	392	2	AX210429	AX210429 Sequence	155	6	85.7	1084	2	CS211757	CS211757 Sequence
C 83	6	85.7	447	2	AR443227	AR443227 Sequence	156	6	85.7	1084	6	CYU12420	UI2420 Cricetus
C 84	6	85.7	447	2	CQ777557	CQ777557 Sequence	157	6	85.7	1086	6	AY157969	AY157969 Rattus no
C 85	6	85.7	448	7	HSC11106	AL158267 H.sapiens	158	6	85.7	1116	2	AR375733	AR375733 Sequence
C 86	6	85.7	461	2	CQ921909	CQ921909 Sequence	C 159	6	85.7	1116	2	AX654406	AX654406 Sequence
C 87	6	85.7	469	2	CQ295969	CQ295969 Sequence	C 160	6	85.7	1128	2	AR375035	AR375035 Sequence
C 88	6	85.7	477	13	AY598732	AY598732 Eulalia v	C 161	6	85.7	1142	11	CR390944	CR390944 Gallus ga
C 89	6	85.7	480	7	G34628	G34628 human SRS s	C 162	6	85.7	1198	11	AX950293	AX950293 Gallus ga
C 90	6	85.7	491	7	G99807	G99807 S208P6061PC	C 163	6	85.7	1216	2	AR170810	AR170810 Sequence
C 91	6	85.7	497	2	G99807	AX988217 Sequence	C 164	6	85.7	1250	13	TFU85621	TFU85621 Trichomo
C 92	6	85.7	497	2	BD123076	BD123076 EST and e	C 165	6	85.7	1285	6	MMYORF	MMYORF Mouse y chr
C 93	6	85.7	497	2	AR427523	AR427523 Sequence	C 166	6	85.7	1321	13	AY617385	AY617385 Sterkiell
C 94	6	85.7	511	7	BV292235	BV292235 S232P6459	C 167	6	85.7	1378	14	AY377346	AY377346 Gulo gulo
C 95	6	85.7	517	2	BD151138	BD151138 Primer fo	C 168	6	85.7	1380	13	AF100647	AF100647 Trypanoso
C 96	6	85.7	517	2	CQ717985	CQ717985 Sequence	C 169	6	85.7	1436	2	AX025512	AX025512 Sequence
C 97	6	85.7	517	2	AX871076	AX871076 Sequence	C 170	6	85.7	1436	2	AX025512	AX025512 Sequence
C 98	6	85.7	541	2	AX210455	AX210455 Sequence	C 171	6	85.7	1452	5	HSU63108	HSU63108 Human eukar
C 99	6	85.7	553	7	G90457	G90457 S208P6416RE	C 172	6	85.7	1485	4	RICMTB2	RICMTB2 Oryza sativ
C 100	6	85.7	566	7	BV103893	BV103893 MARC 4607	C 173	6	85.7	1539	2	AX463562	AX463562 Sequence
C 101	6	85.7	574	2	CQ101506	CQ101506 Sequence	C 174	6	85.7	1546	4	MIOSEPLB2	MIOSEPLB2 Rrice mitoch
C 102	6	85.7	574	2	CQ140501	CQ140501 Sequence	C 175	6	85.7	1591	2	BD160574	BD160574 Primer fo
C 103	6	85.7	574	2	CQ223819	CQ223819 Sequence	C 176	6	85.7	1591	2	AX883862	AX883862 Sequence
C 104	6	85.7	574	2	CQ261806	CQ261806 Sequence	C 177	6	85.7	1591	2	AX883862	AX883862 Sequence
C 105	6	85.7	574	2	CQ299052	CQ299052 Sequence	C 178	6	85.7	1605	2	E64409	E64409 Peptide hav
C 106	6	85.7	574	2	CQ335968	CQ335968 Sequence	C 179	6	85.7	1605	2	AX210627	AX210627 Sequence
C 107	6	85.7	580	7	MMU50414	U50414 Mus musculur	C 180	6	85.7	1647	4	DQ056727	DQ056727 Homo sapi
C 108	6	85.7	589	7	BV356736	BV356736 S231P668R	C 181	6	85.7	1683	5	BC043226	BC043226 Homo sapi
C 109	6	85.7	596	6	AB038243	AB038243 Mus muscu	C 182	6	85.7	1694	5	BC032406	BC032406 Homo sapi
C 110	6	85.7	613	7	BV068865	BV068865 S212P6320	C 183	6	85.7	1743	4	AK067423	AK067423 Oryza sat
C 111	6	85.7	632	7	BV356359	BV356359 S231P6201	C 184	6	85.7	1748	6	BC079216	BC079216 Rattus no
C 112	6	85.7	660	2	BD162314	BD162314 Novel pol	C 185	6	85.7	1755	13	AY060295	AY060295 Drocephil
C 113	6	85.7	660	2	AX120197	AX120197 Sequence	C 186	6	85.7	1802	5	BC024183	BC024183 Homo sapi
C 114	6	85.7	669	7	BV078027	BV078027 S212P6035	C 187	6	85.7	1802	5	BC034491	BC034491 Homo sapi
C 115	6	85.7	672	2	AR764881	AR764881 Sequence	C 188	6	85.7	1829	13	EZ08TUB	EZ08TUB Encephalito
C 116	6	85.7	681	2	BD149055	BD149055 Primer fo	C 189	6	85.7	1834	6	AB016768	AB016768 Mus muscu
C 117	6	85.7	681	2	AX868993	AX868993 Sequence	C 190	6	85.7	1834	6	AB016768	AB016768 Mus muscu
C 118	6	85.7	691	14	DQ218446	DQ218446 Sus scrof	C 191	6	85.7	1848	14	BC111324	BC111324 Bos tauru
C 119	6	85.7	693	7	BV252516	BV252516 S234P6375	C 192	6	85.7	1886	6	BC027256	BC027256 Mus muscu
C 120	6	85.7	710	7	BV501024	BV501024 S222P6206	C 193	6	85.7	1898	2	BD159969	BD159969 Primer fo
C 121	6	85.7	724	10	AB167995	AB167995 Human ech	C 194	6	85.7	1898	2	AX882860	AX882860 Sequence
C 122	6	85.7	726	11	CAM290505	AJ290505 Carlia am	C 195	6	85.7	1898	5	AX023362	AX023362 Homo sapi
C 123	6	85.7	730	11	BX930880	BX930880 Gallus ga	C 196	6	85.7	1913	5	AX023362	AX023362 Homo sapi
C 124	6	85.7	731	11	BX933282	BX933282 Gallus ga	C 197	6	85.7	1931	5	AX023362	AX023362 Homo sapi
C 125	6	85.7	746	11	BX933329	BX933329 Gallus ga	C 198	6	85.7	1960	5	HSM5H3	HSM5H3 Macaca fa
C 126	6	85.7	749	2	BD220724	BD220724 Human gen	C 199	6	85.7	1981	5	AX056166	AX056166 Homo sapi
C 127	6	85.7	751	5	HS324854	AJ324854 Homo sapi	C 200	6	85.7	2000	2	AX509675	AX509675 Sequence
C 128	6	85.7	775	7	BV484934	BV484934 S215P6147	C 201	6	85.7	2000	2	AX52380	AX52380 Sequence
C 129	6	85.7	782	7	BV496165	BV496165 S217P6147	C 202	6	85.7	2014	11	BC076289	BC076289 Danio rer
C 130	6	85.7	788	7	BV633139	BV633139 S216P6218	C 203	6	85.7	2119	6	BC051106	BC051106 Mus muscu
C 131	6	85.7	790	4	AY183020	AY183020 Trifolium	C 204	6	85.7	2175	2	DD164600	DD164600 NOVEL COM
C 132	6	85.7	802	7	BV456636	BV456636 S217P6192	C 205	6	85.7	2175	2	AX695820	AX695820 Sequence
C 133	6	85.7	804	5	HSM5HV6	AF070077 Homo sapi	C 206	6	85.7	2179	13	AF003342	AF003342 Drocephil
C 134	6	85.7	814	7	BV649478	BV649478 S216P6142	C 207	6	85.7	2209	2	BD159066	BD159066 Primer fo
C 135	6	85.7	835	4	AF162210	AF162210 Lactuca s	C 208	6	85.7	2209	2	AX881484	AX881484 Sequence
C 136	6	85.7	836	7	BV612195	BV612195 S217P6150	C 209	6	85.7	2209	5	AX021622	AX021622 Homo sapi
C 137	6	85.7	837	7	BV618122	BV618122 S217P6186	C 210	6	85.7	2215	2	BD157411	BD157411 Primer fo
C 138	6	85.7	846	6	BC054440	BC054440 Mus muscu	C 211	6	85.7	2215	2	AX878726	AX878726 Sequence
C 139	6	85.7	857	7	BV4833129	BV4833129 s1x14f03	C 212	6	85.7	2215	5	AX021844	AX021844 Homo sapi
C 140	6	85.7	864	7	CNS06K5L	AL402463 t7 end of	C 213	6	85.7	2229	7	BV178520	BV178520 sqm10107
C 141	6	85.7	870	2	BD249974	BD249974 50 human	C 214	6	85.7	2252	5	HSU41448	HSU41448 Homo sapien
C 142	6	85.7	870	2	BV520464	BV520464 C591P6455	C 215	6	85.7	2276	4	CAR250836	CAR250836 Cicer ari
C 143	6	85.7	880	6	BC013618	BC013618 Mus muscu	C 216	6	85.7	2353	5	BC035166	BC035166 Homo sapi
C 144	6	85.7	883	11	AY626691	AY626691 Saprosin	C 217	6	85.7	2418	5	AB063085	AB063085 Macaca fa
C 145	6	85.7	883	11	AY626692	AY626692 Saprosin	C 218	6	85.7	2422	5	BC063873	BC063873 Homo sapi
C 146	6	85.7	884	7	BV467774	BV467774 C591P6001	C 219	6	85.7	2422	5	AX092325	AX092325 Homo sapi
C 147	6	85.7	888	11	BX930800	BX930800 Gallus ga	C 220	6	85.7	2514	6	RNU84612	RNU84612 Rattus norv
C 148	6	85.7	888	11	BX930832	BX930832 Gallus ga	C 221	6	85.7	2541	11	AY735397	AY735397 Danio rer
C 149	6	85.7	892	2	AR671031	AR671031 Sequence	C 222	6	85.7	2566	2	BD159659	BD159659 Primer fo

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 12, 2006, 20:46:38 ; Search time 164 Seconds
(without alignments)
119.628 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 37

Sequence: 1 YLTQPOS 7

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 2395520 seqs, 934235491 residues

Total number of hits satisfying chosen parameters: 4791040

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Command line parameters:

-MODEL=frame_p2n.model -DSV=xlh

-Q=/abss/ABSSWEB_spool/US10537648/runat_12102006_151437_15215/app_query.fasta.1

-DB=Published Applications NA_New -QMT=fastcap -SUFFIX=p2n.rnpbn -MINMATCH=0.1

-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blsum62

-TRANS=human40.cdi -LIST=1000 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100

-THR MIN=0 -ALIGN=100 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500

-MINLEN=0 -MAXLEN=2000000000 -HOST=abs03h

-USER=US10537648 @CGN_1_1_238 @runat_12102006_151437_15215 -NCPU=6 -ICPU=3

-NO WMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120

-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7

-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*

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10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	34	91.9	864	8	US-11-266-748A-369640
3	34	91.9	864	8	US-11-266-748A-453019
4	34	91.9	2000	7	US-11-299-286-4370
5	34	91.9	59637	6	US-10-539-228-311
6	34	91.9	124074	8	US-11-266-748A-28242
7	34	91.9	128963	6	US-10-540-898-86
8	34	91.9	128963	6	US-10-540-898-86

Sequence 21, Appl
Sequence 181503,
Sequence 172570,
Sequence 229588,
Sequence 88725, A
Sequence 141536,
Sequence 84513, A
Sequence 111869,
Sequence 137324,
Sequence 40157, A
Sequence 40156, A
Sequence 197849,
Sequence 69213, A
Sequence 122024,
Sequence 173755,
Sequence 186472,
Sequence 193735,
Sequence 57572, A
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Sequence 26861, A
Sequence 56273, A
Sequence 414, App
Sequence 526, App
Sequence 658, App
Sequence 69, Appl
Sequence 139, App
Sequence 15474, A
Sequence 28043, A
Sequence 9198, Ap
Sequence 6, Appl
Sequence 105136,
Sequence 116375,
Sequence 37813, A
Sequence 187888,
Sequence 242100,
Sequence 7, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 492, App
Sequence 29071, A
Sequence 28884, A
Sequence 32, Appl
Sequence 805, App
Sequence 848, App
Sequence 59424, A
Sequence 22658, A
Sequence 1232, Ap
Sequence 1, Appl
Sequence 372269,
Sequence 372270,
Sequence 58280, A
Sequence 79854, A
Sequence 132665,
Sequence 8419, Ap
Sequence 202121,
Sequence 202914,
Sequence 204922,
Sequence 78981, A
Sequence 131792,
Sequence 79855, A
Sequence 132666,
Sequence 75660, A
Sequence 7754, Ap
Sequence 15692, A
Sequence 3310, Ap
Sequence 8418, Ap
Sequence 4314, Ap
Sequence 7573, Ap
Sequence 17223, A
Sequence 399, App
Sequence 11422, A
Sequence 362642,
Sequence 446021,

C 81	31	83.8	2713	6	US-10-449-902-21193	Sequence 21193, A	C 154	30	81.1	1000	8	US-11-266-748A-196663	Sequence 196663,
C 82	31	83.8	2824	8	US-11-293-697-1307	Sequence 1307, Ap	C 155	30	81.1	1000	8	US-11-266-748A-199525	Sequence 199525,
C 83	31	83.8	3141	8	US-11-266-748A-23592	Sequence 23592, A	C 156	30	81.1	1000	8	US-11-266-748A-202243	Sequence 202243,
C 84	31	83.8	3472	9	US-11-218-305-22603	Sequence 22603, A	C 157	30	81.1	1000	8	US-11-266-748A-203661	Sequence 203661,
C 85	31	83.8	5087	6	US-10-517-441-594	Sequence 594, App	C 158	30	81.1	1000	8	US-11-266-748A-221613	Sequence 221613,
C 86	31	83.8	5087	6	US-10-517-441-654	Sequence 654, App	C 159	30	81.1	1000	8	US-11-266-748A-222435	Sequence 222435,
C 87	31	83.8	15225	6	US-10-934-003-2	Sequence 2, Appli	C 160	30	81.1	1000	8	US-11-266-748A-223483	Sequence 223483,
C 88	31	83.8	80988	6	US-10-669-920-261	Sequence 261, App	C 161	30	81.1	1000	8	US-11-266-748A-283012	Sequence 283012,
C 89	31	83.8	95963	9	US-11-021-837-39	Sequence 39, Appl	C 162	30	81.1	1000	8	US-11-266-748A-288654	Sequence 288654,
C 90	31	83.8	101954	6	US-10-539-228-782	Sequence 782, App	C 163	30	81.1	1000	8	US-11-266-748A-309652	Sequence 309652,
C 91	31	83.8	107543	6	US-10-539-228-706	Sequence 706, App	C 164	30	81.1	1000	8	US-11-266-748A-340083	Sequence 340083,
C 92	31	83.8	110799	6	US-10-540-898-790	Sequence 790, App	C 165	30	81.1	1000	8	US-11-266-748A-342542	Sequence 342542,
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C 94	31	83.8	215126	6	US-10-540-898-339	Sequence 339, App	C 167	30	81.1	1000	8	US-11-266-748A-397222	Sequence 397222,
C 95	31	83.8	365720	6	US-10-669-920-1267	Sequence 1267, App	C 168	30	81.1	1000	8	US-11-266-748A-399561	Sequence 399561,
C 96	31	83.8	909203	8	US-11-266-748A-23039	Sequence 23039, A	C 169	30	81.1	1000	8	US-11-266-748A-402494	Sequence 402494,
C 97	31	83.8	1320443	6	US-10-833-833-77	Sequence 77, Appl	C 170	30	81.1	1000	8	US-11-266-748A-468268	Sequence 468268,
C 98	31	81.1	48	7	US-11-434-137-11221	Sequence 11221, A	C 171	30	81.1	1000	8	US-11-266-748A-470607	Sequence 470607,
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C 103	30	81.1	306	8	US-11-266-748A-59976	Sequence 59976, A	C 176	30	81.1	1019	9	US-11-056-355B-57641	Sequence 57641, A
C 104	30	81.1	354	8	US-11-266-748A-2477	Sequence 2477, Ap	C 177	30	81.1	1024	8	US-11-266-748A-257846	Sequence 257846,
C 105	30	81.1	354	8	US-11-266-748A-62972	Sequence 62972, A	C 178	30	81.1	1024	8	US-11-266-748A-278254	Sequence 278254,
C 106	30	81.1	354	8	US-11-266-748A-65804	Sequence 65804, A	C 179	30	81.1	1024	8	US-11-266-748A-318363	Sequence 318363,
C 107	30	81.1	385	7	US-11-314-834-2038	Sequence 2038, Ap	C 180	30	81.1	1026	8	US-11-266-748A-368643	Sequence 368643,
C 108	30	81.1	415	8	US-11-266-748A-37093	Sequence 37093, A	C 181	30	81.1	1026	8	US-11-266-748A-452022	Sequence 452022,
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C 112	30	81.1	461	6	US-10-834-268-3109	Sequence 3109, Ap	C 185	30	81.1	1169	8	US-11-266-748A-85732	Sequence 85732, A
C 113	30	81.1	469	8	US-11-266-748A-60751	Sequence 60751, A	C 186	30	81.1	1169	8	US-11-266-748A-112073	Sequence 112073,
C 114	30	81.1	486	8	US-11-266-748A-212034	Sequence 212034, A	C 187	30	81.1	1169	8	US-11-266-748A-138543	Sequence 138543,
C 115	30	81.1	486	8	US-11-266-748A-235549	Sequence 235549, A	C 188	30	81.1	1281	8	US-11-266-748A-362449	Sequence 362449,
C 116	30	81.1	500	8	US-11-266-748A-38188	Sequence 38188, A	C 189	30	81.1	1281	8	US-11-266-748A-445828	Sequence 445828,
C 117	30	81.1	505	8	US-11-266-748A-385441	Sequence 385441, A	C 190	30	81.1	1291	8	US-11-266-748A-20657	Sequence 20657, A
C 118	30	81.1	505	8	US-11-266-748A-448820	Sequence 448820, A	C 191	30	81.1	1345	8	US-11-216-545-1473	Sequence 1473, Ap
C 119	30	81.1	508	8	US-11-266-748A-269980	Sequence 269980, A	C 192	30	81.1	1368	6	US-10-449-902-18929	Sequence 18929, Ap
C 120	30	81.1	508	8	US-11-266-748A-330497	Sequence 330497, A	C 193	30	81.1	1441	8	US-11-266-748A-79600	Sequence 79600, A
C 121	30	81.1	522	6	US-10-834-268-4547	Sequence 4547, Ap	C 194	30	81.1	1441	8	US-11-266-748A-132411	Sequence 132411,
C 122	30	81.1	535	6	US-10-834-268-549	Sequence 549, App	C 195	30	81.1	1515	6	US-10-539-450-3	Sequence 3, Appli
C 123	30	81.1	544	8	US-11-266-748A-377797	Sequence 377797, A	C 196	30	81.1	1515	6	US-11-218-305-23692	Sequence 23692, A
C 124	30	81.1	544	8	US-11-266-748A-461176	Sequence 461176, A	C 197	30	81.1	1614	9	US-11-056-355B-78416	Sequence 78416, A
C 125	30	81.1	569	8	US-11-266-748A-55250	Sequence 55250, A	C 198	30	81.1	1661	6	US-10-449-902-8619	Sequence 8619, Ap
C 126	30	81.1	570	8	US-11-266-748A-182936	Sequence 182936, A	C 199	30	81.1	1696	6	US-10-449-902-27800	Sequence 27800, Ap
C 127	30	81.1	571	7	US-11-292-078-9594	Sequence 9594, Ap	C 200	30	81.1	1743	6	US-10-449-902-15954	Sequence 15954, A
C 128	30	81.1	584	8	US-11-266-748A-44818	Sequence 44818, A	C 201	30	81.1	1771	8	US-11-266-748A-258221	Sequence 258221,
C 129	30	81.1	600	8	US-11-266-748A-47673	Sequence 47673, A	C 202	30	81.1	1771	8	US-11-266-748A-318738	Sequence 318738,
C 130	30	81.1	669	8	US-11-266-748A-209838	Sequence 209838, A	C 203	30	81.1	1771	8	US-10-449-902-2462	Sequence 2462, Ap
C 131	30	81.1	669	8	US-11-266-748A-234204	Sequence 234204, A	C 204	30	81.1	1808	6	US-11-217-525-4544	Sequence 4544, Ap
C 132	30	81.1	731	8	US-11-266-748A-213768	Sequence 213768, A	C 205	30	81.1	1875	8	US-11-056-355B-43332	Sequence 43332, A
C 133	30	81.1	731	8	US-11-266-748A-236614	Sequence 236614, A	C 206	30	81.1	1876	9	US-11-218-305-3943	Sequence 3943, Ap
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C 135	30	81.1	752	8	US-11-266-748A-119314	Sequence 119314, A	C 208	30	81.1	1964	6	US-11-266-748A-22692	Sequence 22692, A
C 136	30	81.1	752	8	US-11-266-748A-161478	Sequence 161478, A	C 209	30	81.1	2040	8	US-11-266-748A-69031	Sequence 69031, A
C 137	30	81.1	752	8	US-11-266-748A-295271	Sequence 295271, A	C 210	30	81.1	2061	8	US-11-266-748A-105202	Sequence 105202,
C 138	30	81.1	752	8	US-11-266-748A-346700	Sequence 346700, A	C 211	30	81.1	2061	8	US-11-266-748A-121842	Sequence 121842,
C 139	30	81.1	775	8	US-11-266-748A-54644	Sequence 54644, A	C 212	30	81.1	2137	6	US-11-218-305-12454	Sequence 12454, A
C 140	30	81.1	803	8	US-11-266-748A-85968	Sequence 85968, A	C 213	30	81.1	2152	6	US-10-449-902-22192	Sequence 22192, A
C 141	30	81.1	803	8	US-11-266-748A-138779	Sequence 138779, A	C 214	30	81.1	2181	8	US-11-293-697-2426	Sequence 2426, Ap
C 142	30	81.1	837	8	US-11-266-748A-86843	Sequence 86843, A	C 215	30	81.1	2181	8	US-11-266-748A-61640	Sequence 61640, Ap
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C 145	30	81.1	849	8	US-11-266-748A-453503	Sequence 453503, A	C 218	30	81.1	2284	8	US-11-266-748A-121840	Sequence 121840,
C 146	30	81.1	873	8	US-11-266-748A-180185	Sequence 180185, A	C 219	30	81.1	2284	8	US-11-266-748A-121840	Sequence 121840,
C 147	30	81.1	873	8	US-11-266-748A-191504	Sequence 191504, A	C 220	30	81.1	2406	8	US-11-056-355B-3713	Sequence 3713, Ap
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C 149	30	81.1	980	8	US-11-266-748A-266484	Sequence 266484, A	C 222	30	81.1	2686	9	US-11-266-748A-112438	Sequence 112438,
C 150	30	81.1	980	8	US-11-266-748A-327001	Sequence 327001, A	C 223	30	81.1	2692	8	US-11-266-748A-186785	Sequence 186785,
C 151	30	81.1	987	6	US-10-449-902-2809	Sequence 2809, Ap	C 224	30	81.1	2692	8	US-11-266-748A-139318	Sequence 139318,
C 152	30	81.1	1000	8	US-11-266-748A-117171	Sequence 117171, A	C 225	30	81.1	2692	8	US-11-266-748A-241527	Sequence 241527,
C 153	30	81.1	1000	8	US-11-266-748A-159335	Sequence 159335, A	C 226	30	81.1	2727	8	US-11-266-748A-352328	Sequence 352328,

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 12, 2006, 20:46:08 ; Search time 1456 Seconds
(without alignments)
88.613 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 37

Sequence: 1 YLTPQPS 7

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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35	94.6	710	7	US-10-027-632-116039, Sequence 116039,
35	94.6	147300	10	US-10-723-681-3, Sequence 3, Appli
35	94.6	147300	10	US-10-857-780-3, Sequence 3, Appli
34	91.9	595	4	US-09-925-065A-588388, Sequence 588388,
34	91.9	595	4	US-09-925-065A-588389, Sequence 588389,
34	91.9	595	4	US-09-925-065A-588390, Sequence 588390,
34	91.9	595	5	US-09-925-065A-588388, Sequence 588388,
34	91.9	595	5	US-09-925-065A-588389, Sequence 588389,
34	91.9	595	5	US-09-925-065A-588390, Sequence 588390,
34	91.9	866	8	US-10-437-963-24461, Sequence 24461, A
34	91.9	866	8	US-10-106-698-12461, Sequence 12461, A
34	91.9	892	4	US-10-653-047-532, Sequence 532, App
34	91.9	892	4	US-09-925-065A-67296, Sequence 67296, A
34	91.9	892	4	US-09-925-065A-67297, Sequence 67297, A
34	91.9	892	5	US-09-925-065A-67296, Sequence 67296, A
34	91.9	892	5	US-09-925-065A-67297, Sequence 67297, A
34	91.9	938	12	US-10-301-480-168535, Sequence 168535,
34	91.9	938	12	US-10-301-480-168536, Sequence 168536,
34	91.9	938	12	US-10-301-480-781944, Sequence 781944,
34	91.9	938	12	US-10-301-480-781945, Sequence 781945,
34	91.9	1026	9	US-10-767-795-5547, Sequence 5547, App
34	91.9	1354	3	US-09-822-846-316, Sequence 316, App
34	91.9	2000	3	US-09-938-842A-4370, Sequence 4370, App
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34	91.9	2000	3	US-09-938-842A-4370, Sequence 4370, App
34	91.9	2448	8	US-10-149-310-193, Sequence 193, App
34	91.9	2448	8	US-10-149-310-193, Sequence 193, App
34	91.9	3953	9	US-10-739-930-279, Sequence 279, App
34	91.9	5379	7	US-10-311-455-303, Sequence 303, App
34	91.9	59637	8	US-10-322-281-311, Sequence 311, App
34	91.9	128963	11	US-10-330-773-86, Sequence 86, Appl
34	91.9	295096	6	US-10-087-192-331, Sequence 331, App
34	91.9	2731748	8	US-10-297-465A-1, Sequence 1, Appli
34	89.2	25	9	US-10-719-993-702816, Sequence 702816,
34	89.2	25	11	US-10-932-182A-181503, Sequence 181503,
34	89.2	201	9	US-10-719-993-4501, Sequence 4501, App
34	89.2	201	9	US-10-719-993-4507, Sequence 4507, App
34	89.2	201	9	US-10-719-993-4528, Sequence 4528, App
34	89.2	201	9	US-10-719-993-4534, Sequence 4534, App
34	89.2	201	9	US-10-719-993-4557, Sequence 4557, App
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34	89.2	201	9	US-10-719-993-4587, Sequence 4587, App
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34	89.2	201	9	US-10-719-993-4614, Sequence 4614, App
34	89.2	201	9	US-10-719-993-4620, Sequence 4620, App
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34	89.2	201	16	US-11-124-367A-2566, Sequence 2566, App
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34	89.2	201	16	US-11-124-367A-2583, Sequence 2583, App
34	89.2	201	16	US-11-124-367A-2588, Sequence 2588, App
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34	89.2	201	16	US-11-124-367A-2632, Sequence 2632, App
34	89.2	201	16	US-11-124-367A-2656, Sequence 2656, App
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34	89.2	201	16	US-11-124-367A-2672, Sequence 2672, App
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34	89.2	201	16	US-11-124-367A-2688, Sequence 2688, App
34	89.2	201	16	US-11-124-367A-2690, Sequence 2690, App
34	89.2	251	9	US-10-425-115-166919, Sequence 166919,
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34	89.2	506	4	US-09-925-065A-760214, Sequence 760214,
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C 76	33	89.2	506	5	US-09-925-065A-760214	Sequence 760214,	149	33	89.2	996	7	US-10-369-493-24791	Sequence 24791, A
C 77	33	89.2	506	5	US-09-925-065A-760215	Sequence 760215,	150	33	89.2	1082	4	US-09-925-065A-720088	Sequence 720088,
C 78	33	89.2	506	5	US-10-301-480-277141	Sequence 277141,	151	33	89.2	1082	5	US-09-925-065A-720088	Sequence 720088,
C 79	33	89.2	518	12	US-10-301-480-890550	Sequence 890550,	152	33	89.2	1216	2	US-08-838-151A-62	Sequence 62, Appl
C 80	33	89.2	523	4	US-09-925-065A-475527	Sequence 475527,	153	33	89.2	1242	11	US-10-932-182A-173755	Sequence 173755,
C 81	33	89.2	523	4	US-09-925-065A-475528	Sequence 475528,	154	33	89.2	1333	7	US-10-017-161-463	Sequence 463, App
C 82	33	89.2	523	4	US-09-925-065A-475529	Sequence 475529,	155	33	89.2	1333	7	US-10-017-161-473	Sequence 473, App
C 83	33	89.2	523	5	US-09-925-065A-475527	Sequence 475527,	156	33	89.2	1333	7	US-10-292-798-257	Sequence 257, App
C 84	33	89.2	523	5	US-09-925-065A-475528	Sequence 475528,	157	33	89.2	1371	4	US-09-925-065A-703088	Sequence 703088,
C 85	33	89.2	523	5	US-09-925-065A-475529	Sequence 475529,	158	33	89.2	1371	4	US-09-925-065A-703088	Sequence 703088,
C 86	33	89.2	530	4	US-09-925-065A-187047	Sequence 187047,	159	33	89.2	1371	5	US-09-925-065A-703088	Sequence 703088,
C 87	33	89.2	530	5	US-09-925-065A-187047	Sequence 187047,	160	33	89.2	1371	5	US-09-925-065A-703088	Sequence 703088,
C 88	33	89.2	543	4	US-09-925-065A-793236	Sequence 793236,	161	33	89.2	1943	8	US-10-221-278-492	Sequence 492, App
C 89	33	89.2	543	5	US-09-925-065A-793236	Sequence 793236,	162	33	89.2	1943	8	US-10-221-278-492	Sequence 492, App
C 90	33	89.2	546	8	US-10-424-599-47073	Sequence 47073, A	163	33	89.2	2178	10	US-10-501-282-2353	Sequence 2353, App
C 91	33	89.2	563	4	US-09-925-065A-193774	Sequence 193774,	164	33	89.2	2178	10	US-10-501-282-2355	Sequence 2355, App
C 92	33	89.2	563	5	US-09-925-065A-193774	Sequence 193774,	165	33	89.2	2178	10	US-10-501-282-2355	Sequence 2355, App
C 93	33	89.2	567	12	US-10-301-480-446793	Sequence 446793,	166	33	89.2	2659	9	US-10-483-512-109	Sequence 109, App
C 94	33	89.2	567	12	US-10-301-480-446794	Sequence 446794,	167	33	89.2	2659	9	US-10-483-512-109	Sequence 109, App
C 95	33	89.2	567	12	US-10-301-480-1060202	Sequence 1060202,	168	33	89.2	2798	6	US-10-027-632-76176	Sequence 76176, A
C 96	33	89.2	567	12	US-10-301-480-1060203	Sequence 1060203,	169	33	89.2	2798	6	US-10-027-632-76176	Sequence 76176, A
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C 98	33	89.2	568	5	US-09-925-065A-372545	Sequence 372545,	171	33	89.2	3242	8	US-10-437-963-19043	Sequence 19043, A
C 99	33	89.2	572	4	US-09-925-065A-377351	Sequence 377351,	172	33	89.2	4256	9	US-10-719-993-319	Sequence 319, App
C 100	33	89.2	572	4	US-09-925-065A-377352	Sequence 377352,	173	33	89.2	4256	9	US-10-719-993-319	Sequence 319, App
C 101	33	89.2	572	5	US-09-925-065A-377351	Sequence 377351,	174	33	89.2	4779	13	US-11-097-143-24139	Sequence 24139, A
C 102	33	89.2	572	5	US-09-925-065A-377352	Sequence 377352,	175	33	89.2	4779	13	US-11-097-143-24139	Sequence 24139, A
C 103	33	89.2	573	12	US-10-301-480-283164	Sequence 283164,	176	33	89.2	4803	10	US-10-956-157-1094	Sequence 1094, App
C 104	33	89.2	573	12	US-10-301-480-896573	Sequence 896573,	177	33	89.2	4803	10	US-10-956-157-1094	Sequence 1094, App
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C 106	33	89.2	633	12	US-10-301-480-437542	Sequence 437542,	179	33	89.2	5924	6	US-11-041-856-2	Sequence 2, Appl
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C 108	33	89.2	635	4	US-09-925-065A-81183	Sequence 81183, A	181	33	89.2	5957	9	US-10-719-993-320	Sequence 320, App
C 109	33	89.2	635	5	US-09-925-065A-81183	Sequence 81183, A	182	33	89.2	5957	9	US-10-719-993-320	Sequence 320, App
C 110	33	89.2	635	12	US-10-301-480-182422	Sequence 182422,	183	33	89.2	6107	16	US-11-124-367A-136	Sequence 136, App
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C 112	33	89.2	636	4	US-09-925-065A-367198	Sequence 367198,	185	33	89.2	6179	16	US-10-719-993-318	Sequence 318, App
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47	826	14	AG866816
c	48	37	100.0
49	854	12	CC541008
c	50	37	100.0
51	859	12	CG818959
c	52	37	100.0
53	870	14	AG896133
c	54	37	100.0
55	987	14	CNS047BX
c	56	37	100.0
57	103	12	CC399803
c	58	37	100.0
59	213	5	CF492357
c	60	37	100.0
61	233	1	AV291967
c	62	37	100.0
63	257	12	CG733995
c	64	37	100.0
65	316	5	CF493005
c	66	37	100.0
67	371	5	CF492527
c	68	37	100.0
69	375	5	CF492849
c	70	37	100.0
71	380	5	CF492337
c	72	37	100.0
73	397	5	CF492607
c	74	37	100.0
75	419	5	CF492431
c	76	37	100.0
77	425	2	B1927985
c	78	37	100.0
79	427	5	CF492433
c	80	37	100.0
81	445	5	CF492826
c	82	37	100.0
83	479	5	CF492873
c	84	37	100.0
85	484	5	CF492824
c	86	37	100.0
87	484	5	CF492825
c	88	37	100.0
89	486	3	B2900496
c	90	37	100.0
91	515	5	CF492077
c	92	37	100.0
93	590	5	CF493012
c	94	37	100.0
95	611	5	CF492583
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97	626	5	CF492131
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99	634	12	CE525160
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101	660	5	CF491904
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103	691	3	B283824
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107	712	14	AG104428
c	108	37	100.0
109	718	12	CG192771
c	110	37	100.0
111	720	5	CF492229
c	112	37	100.0
113	737	12	CG280520
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117	765	12	CC693830
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119	777	12	BZ642496
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121	803	10	DV533421
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123	809	10	DM145071
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125	812	11	BH201530
c	126	37	100.0
127	843	12	BZ734651
c	128	37	100.0
129	872	10	DM145668
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131	877	3	BQ882260
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133	879	12	BZ749475
c	134	37	100.0
135	936	13	DU071393
c	136	37	100.0
137	950	12	CG237923
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139	991	120	3
c	140	37	100.0
141	125	3	BM725400
c	142	37	100.0
143	225	2	BI003642

DA534392	DA534392
CZ638826	OM_BA018
AQ252207	HS_3184_A
DE130155	Oryzias_1
CR176637	Reverse s
CR192824	Reverse s
AQ464802	HS_5105_B
CR260251	Reverse s
CR251702	Reverse s
BJ838064	BJ838064
BZ879825	CH240_293
BJ826782	BJ826782
BZ291378	CH240_119
AQ077211	CIT-HSP-2
BJ830318	BJ830318
CR149426	Reverse s
AG494285	Mus muscu
BH598970	BOGVELITP
EX966213	Reverse s
CR130680	Reverse s
CT047189	Sus scrofa
BH064279	RPTC-24-3
CL831140	OR_CBA005
CG674428	trb2160 t
AG866816	Oryza sat
CC541008	CH240_421
CG818959	SOYCD72TH
AG896133	Oryza sat
AL277782	Tetraodon
CC399803	FUHDK10TD
CF492357	NG1-00457
AV291967	AV291967
CG733995	1119161E1
CF493005	MS1-0131U
CF492527	ML1-0080T
CF492849	MS1-0063U
CF492337	MS1-0024U
CF492607	MS1-0106T
CF492431	MS1-0106T
B1927985	EST547862
CF492433	MS1-0106T
CF492826	MS1-0060G
CF492873	MS1-0063U
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CF492131	ME1-0005T
CF525160	tigr-gss-
CF491904	MA1-0024G
B283824	603867958
CF492047	MA3-9999U
AG104428	Pan trogl
CG192771	PUGN33TB
CF492229	ME1-0038G
CG280520	OGVDX83TH
CF492057	MA3-9999U
CC693830	OGUBP88TV
BZ642496	OGCAU13TC
DV533421	2M_BFB022
DM145071	CLVX10139
BH201530	Sm1-54H16
BZ734651	OGEDL77TM
DM145668	CLVX10762
BQ882260	AGENCOURT
BZ749475	OGA0A52TC
DU071393	62293_Tom
CG237923	OGCPS5TV
BM725400	UI-B-EJO-
BM677827	UI-B-EJO-
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79	C	79	34	91.9	329	10	FI1225	FI1225 HSC2UB091 n	C 152	34	91.9	890	5	CD302303	CD302303 AGENCOURT
80	C	80	34	91.9	342	2	BF866333	BF866333 PM3-TN010	C 153	34	91.9	905	5	CF241277	CF241277 AGENCOURT
81	C	81	34	91.9	350	14	TA303G070	TA303G070 T. brucei	C 154	34	91.9	916	13	DU204773	DU204773 109857412
82	C	82	34	91.9	414	12	B2761974	B2761974 SALK 0838	C 155	34	91.9	932	11	CNS075WM	CNS075WM CNTHU39TR
83	C	83	34	91.9	431	10	W79925	W79925 z474405.r1	C 156	34	91.9	937	11	AZ681879	AZ681879 ENTHU39TR
84	C	84	34	91.9	434	11	AO556308	AO556308 HS 5223 B	C 157	34	91.9	973	7	BE739456	BE739456 601556253
85	C	85	34	91.9	441	8	CV071393	CV071393 CS_g11_37	C 158	34	91.9	980	14	CNS04WJ9	CNS04WJ9 AL310446 Tetraodon
86	C	86	34	91.9	447	1	AA175629	AA175629 ms9605.r	C 159	34	91.9	1076	7	BE572072	BE572072 601333831
87	C	87	34	91.9	458	14	DE055884	DE055884 Oryzias l	C 160	34	91.9	1361	10	DV798971	DV798971 Hw loain 6
88	C	88	34	91.9	460	11	A2839488	A2839488 2M0135P08	C 161	34	91.9	1553	12	CC286648	CC286648 CH761-16N
89	C	89	34	91.9	461	2	BM421354	BM421354 V008B04 O	C 162	34	91.9	1712	6	HS0802803	HS0802803 QHJ3D02.y
90	C	90	34	91.9	466	13	C2637278	C2637278 OM_BA018	C 163	34	91.9	162	3	BU034130	BU034130 QHJ3D02.y
91	C	91	34	91.9	468	11	AQ004550	AQ004550 CIT-HSP-2	C 164	34	91.9	168	12	CE330633	CE330633 tigr-g88-
92	C	92	34	91.9	468	13	QW12569	QW12569 104_499.1	C 165	34	91.9	170	10	DW364299	DW364299 LI-R-CMO-
93	C	93	34	91.9	470	3	BQ373222	BQ373222 QV1-FT016	C 166	34	91.9	172	10	DF395118	DF395118 UR-R-CMO-
94	C	94	34	91.9	502	12	B2869981	B2869981 CH240_224	C 167	34	91.9	178	2	BM194624	BM194624 TCAAP3Q13
95	C	95	34	91.9	505	2	BF724407	BF724407 bx04e07.y	C 168	34	91.9	188	2	BM194624	BM194624 TCAAP3Q13
96	C	96	34	91.9	508	11	A2060026	A2060026 RPCI-23-4	C 169	34	91.9	201	1	AA376300	AA376300 MCB22F10
97	C	97	34	91.9	516	11	AQ881729	AQ881729 HS 5272_A	C 170	34	91.9	214	1	AA977165	AA977165 OQ25a06.8
98	C	98	34	91.9	525	4	AX109157	AX109157 BX109157	C 171	34	91.9	222	14	DU486164	DU486164 109842109
99	C	99	34	91.9	525	8	CV973830	CV973830 EST00168	C 172	34	91.9	229	1	AV323627	AV323627 AV323627
100	C	100	34	91.9	527	14	DE047882	DE047882 Oryzias l	C 173	34	91.9	241	2	BI054074	BI054074 MR3-GN034
101	C	101	34	91.9	530	10	RI1919	RI1919 yf50109.r1	C 174	34	91.9	244	2	BG588726	BG588726 AV292176
102	C	102	34	91.9	537	7	AW187042	AW187042 ENLGH1912	C 175	34	91.9	250	1	AV292176	AV292176 AV292176
103	C	103	34	91.9	538	1	AA116422	AA116422 mp96e09.r	C 176	34	91.9	254	10	DW187157	DW187157 EST03427
104	C	104	34	91.9	542	1	AA046904	AA046904 zif47d12.r	C 177	34	91.9	254	10	DW187157	DW187157 EST03427
105	C	105	34	91.9	542	1	AA046904	AA046904 zif47d12.r	C 178	34	91.9	254	10	DW187157	DW187157 EST03427
106	C	106	34	91.9	553	8	CN847313	CN847313 PG07031D1	C 179	34	91.9	275	2	BF932956	BF932956 CM1-NT027
107	C	107	34	91.9	559	12	CG811833	CG811833 FSAAE73TF	C 180	34	91.9	280	7	BB112871	BB112871 BB112871
108	C	108	34	91.9	564	7	BE288117	BE288117 601094368	C 181	34	91.9	288	4	BX303555	BX303555 BX303555
109	C	109	34	91.9	571	9	DA723738	DA723738 DA723738	C 182	34	91.9	289	10	DY176384	DY176384 991120BL1
110	C	110	34	91.9	578	7	AV830274	AV830274 AV830274	C 183	34	91.9	291	7	BF560952	BF560952 UI-R-EI-f
111	C	111	34	91.9	578	9	DA488816	DA488816 DA488816	C 184	34	91.9	294	10	DY152116	DY152116 000508FTN
112	C	112	34	91.9	578	9	DA483057	DA483057 DA483057	C 185	34	91.9	296	1	AV086855	AV086855 AV086855
113	C	113	34	91.9	580	12	CE321214	CE321214 tigr-g88-	C 186	34	91.9	336	12	BZ870843	BZ870843 CH240_275
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115	C	115	34	91.9	600	1	AA635507	AA635507 nr36all.8	C 188	34	91.9	343	4	CB693519	CB693519 AMGNNUC.N
116	C	116	34	91.9	616	1	AI134431	AI134431 DKFP547G	C 189	34	91.9	343	4	CB693519	CB693519 AMGNNUC.N
117	C	117	34	91.9	619	7	BF382458	BF382458 601815440	C 190	34	91.9	344	1	AA504187	AA504187 aa58h08.s
118	C	118	34	91.9	634	11	AZ878051	AZ878051 RPCI-23-1	C 191	34	91.9	344	1	AA504187	AA504187 aa58h08.s
119	C	119	34	91.9	643	11	BH304505	BH304505 CH230-85E	C 192	34	91.9	380	5	CJ202747	CJ202747 CJ202747
120	C	120	34	91.9	647	4	CA066990	CA066990 SCJFAD101	C 193	34	91.9	380	5	CJ202747	CJ202747 CJ202747
121	C	121	34	91.9	651	3	BM723856	BM723856 UI-E-E01-	C 194	34	91.9	383	11	B30431	B30431 HS-1001-B1-
122	C	122	34	91.9	651	14	AG063207	AG063207 Pan trogl	C 195	34	91.9	383	11	B30431	B30431 HS-1001-B1-
123	C	123	34	91.9	657	2	BJ625552	BJ625552 BJ625552	C 196	34	91.9	392	1	AA324126	AA324126 EST27019
124	C	124	34	91.9	659	14	DX165808	DX165808 OR_Aba002	C 197	34	91.9	392	5	CF144028	CF144028 UI-HF-BP0
125	C	125	34	91.9	660	11	BH833188	BH833188 BACP4-N1	C 198	34	91.9	393	5	CJ204359	CJ204359 CJ204359
126	C	126	34	91.9	699	5	CD639617	CD639617 AGENCOURT	C 199	34	91.9	393	7	AW494676	AW494676 UI-M-BH3-
127	C	127	34	91.9	701	14	BX126995	BX126995 Danio rer	C 200	34	91.9	394	7	AW494676	AW494676 UI-M-BH3-
128	C	128	34	91.9	703	14	DX015611	DX015611 KBR00710	C 201	34	91.9	395	14	CR158549	CR158549 Forward 8
129	C	129	34	91.9	709	12	CG133113	CG133113 PUFWA03TD	C 202	34	91.9	404	2	BJ062050	BJ062050 uw60e12.y
130	C	130	34	91.9	717	14	AG103444	AG103444 Pan trogl	C 203	34	91.9	404	2	BJ062050	BJ062050 uw60e12.y
131	C	131	34	91.9	719	12	CE062497	CE062497 tigr-g88-	C 204	34	91.9	408	3	BP855374	BP855374 tigr-g88-
132	C	132	34	91.9	721	11	AZ706197	AZ706197 RPCI-23-2	C 205	34	91.9	408	3	BP855374	BP855374 tigr-g88-
133	C	133	34	91.9	727	13	C2432372	C2432372 OA_BBA012	C 206	34	91.9	409	1	AL4705087	AL4705087 DKFZP686F
134	C	134	34	91.9	735	12	CG397615	CG397615 tigr-g88-	C 207	34	91.9	409	1	AL4705087	AL4705087 DKFZP686F
135	C	135	34	91.9	744	9	CG983782	CG983782 JGI_CAAPI	C 208	34	91.9	409	1	AL4705087	AL4705087 DKFZP686F
136	C	136	34	91.9	745	9	CG983782	CG983782 JGI_CAAPI	C 209	34	91.9	411	7	AW527822	AW527822 UI-R-B01-
137	C	137	34	91.9	747	14	AG098613	AG098613 Pan trogl	C 210	34	91.9	411	10	H10691	H10691 YMO7h02.r1
138	C	138	34	91.9	752	5	CF286958	CF286958 AGENCOURT	C 211	34	91.9	412	2	BF742852	BF742852 IL2-BT073
139	C	139	34	91.9	763	14	CT271977	CT271977 Sub_sctof	C 212	34	91.9	412	2	BF742852	BF742852 IL2-BT073
140	C	140	34	91.9	768	9	DB165925	DB165925 DB165925	C 213	34	91.9	415	14	DX252469	DX252469 OR_Aba014
141	C	141	34	91.9	778	3	BM680272	BM680272 UI-E-E01-	C 214	34	91.9	417	8	CN256146	CN256146 170005321
142	C	142	34	91.9	781	12	CG673512	CG673512 tigr1244 t	C 215	34	91.9	417	11	B06411	B06411 CSRLL-80a8-u
143	C	143	34	91.9	791	11	BZ484295	BZ484295 BONHV01TF	C 216	34	91.9	426	11	AQ175294	AQ175294 HS-3210-A
144	C	144	34	91.9	811	7	BF700942	BF700942 602127880	C 217	34	91.9	426	11	AQ175294	AQ175294 HS-3210-A
145	C	145	34	91.9	816	2	BI652561	BI652561 603299470	C 218	34	91.9	426	11	AQ175294	AQ175294 HS-3210-A
146	C	146	34	91.9	818	12	CC926946	CC926946 C092d05ba	C 219	34	91.9	428	10	H12719	H12719 YJ13d12.81
147	C	147	34	91.9	824	14	CR035156	CR035156 Forward s	C 220	34	91.9	428	10	H12719	H12719 YJ13d12.81
148	C	148	34	91.9	826	13	CG968207	CG968207 AIAA-aaao	C 221	34	91.9	428	11	H051904	H051904 RPCI-24-9
149	C	149	34	91.9	827	9	DN261604	DN261604 Meso00114	C 222	34	91.9	428	12	CC055322	CC055322 SALK_0937
150	C	150	34	91.9	864	5	CD516081	CD516081 AGENCOURT	C 223	34	91.9	432	5	CJ204415	CJ204415 CU204415

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 12, 2006, 20:36:29 ; Search time 430 Seconds

(without alignments)
170.253 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 37

Sequence: 1 YLTQPS 7

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Command line parameters: -DEV=xlh

-MODEL=frame_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10537648/runat_12102006_151421_15024/app_query.fasta.1
-DB=N Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1000
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=100 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abes03h
-USER=US10537648@CGN11761@runat_12102006_151421_15024 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_8.*

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2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*
15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	100.0	21	ADQ16436	Adq16436 Nucleic a
2	37	100.0	2000	ADA73402	Ada73402 Rice gene
3	35	94.6	686	AAK57664	Aak57664 Human imm

35	94.6	16098	8	ACC48787	Acc48787 Human Evi
35	94.6	147300	12	ADP45593	Adp45593 Human Rho
35	94.6	147700	14	ADX98570	Adx98570 Human Gua
35	94.6	147700	15	AEE96613	Aee96613 KIAA0861
34	91.9	376	6	ABN19259	Abn19259 Human ORF
34	91.9	866	4	AAH34154	Aah34154 Human col
34	91.9	892	3	AAF08009	Aaf08009 Fusarium
34	91.9	892	13	ADU52050	Adu52050 Fusarium
34	91.9	892	14	ADZ90053	Adz90053 Fusarium
34	91.9	1026	13	ADR64766	Adr64766 Cotton cD
34	91.9	1354	6	ABK35925	Abk35925 cDNA sequ
34	91.9	2000	6	ABZ16565	Abz16565 Arabidops
34	91.9	2000	8	ADA68927	Ada68927 Arabidops
34	91.9	2448	6	ABN79854	Abn79854 Fungal ZB
34	91.9	3953	13	ADT14953	Adt14953 Plant cDN
34	91.9	5379	6	ABL32330	AbL32330 Human imm
34	91.9	5379	13	ABD33270	Abd33270 Murine ca
34	91.9	128963	12	ADQ97110	Adq97110 Human can
34	91.9	242496	14	AED76150	Aed76150 Mouse CA
34	91.9	295096	11	ACN44068	Acn44068 Mouse gen
34	89.2	121	10	ADH92944	Adh92944 Human gen
33	89.2	392	5	AAH81562	Aah81562 Human dif
33	89.2	411	13	ACF86753	Acf86753 Human SIR
33	89.2	492	13	ACF81501	Acf81501 Human SIR
33	89.2	584	10	ADK52858	Adk52858 Plant DNA
33	89.2	996	13	ADS46361	Ads46361 Bacterial
33	89.2	1116	10	ADF00454	Adf00454 Bacterial
33	89.2	1216	2	AAT93320	Aat93320 Tomato-in
33	89.2	1333	10	ADC85804	Adc85804 Human GPC
33	89.2	1539	6	AAH48581	Aah48581 A thalian
33	89.2	1943	5	AAJ45223	Aaj45223 cDNA enco
33	89.2	2178	9	ADB08415	Adb08415 Alloiococ
33	89.2	2178	9	ADB08417	Adb08417 Alloiococ
33	89.2	2178	9	ADB08413	Adb08413 Alloiococ
33	89.2	2569	10	ADC30261	Adc30261 Human nov
33	89.2	2659	9	ABT43745	Abt43745 Molecule
33	89.2	3324	6	AAJ94913	Aaj94913 Human DNA
33	89.2	3999	4	AAJ28025	Aaj28025 Human IKA
33	89.2	3999	4	AAF29756	Aaf29756 Human IKA
33	89.2	4417	13	ADR07102	Adr07102 Full leng
33	89.2	4779	4	ABU17932	Abu17932 Drosophill
33	89.2	4788	4	AAH14533	Aah14533 Human cDN
33	89.2	4803	5	AAH81767	Aah81767 Human dif
33	89.2	4803	6	AAH44190	Aah44190 Human I-k
33	89.2	5924	6	ABQ80570	Abq80570 Mutant hu
33	89.2	5924	6	ABQ80569	Abq80569 Human IKB
33	89.2	5924	8	ACD13384	AcD13384 Human DNA
33	89.2	6699	6	AAJ63320	Aaj63320 Chemicall
33	89.2	7282	4	AAK86318	Aak86318 Human imm
33	89.2	7599	2	AAJ58802	Aaj58802 Human leu
33	89.2	8436	13	ADR84202	Adr84202 Aspergill
33	89.2	18888	4	ABL23020	AbL23020 Drosophill
33	89.2	20689	4	AAH78366	Aah78366 Human imm
33	89.2	32185	11	ACN44604	Acn44604 Mouse gen
33	89.2	39325	4	AAK81660	Aak81660 Human imm
33	89.2	50460	11	ACN44936	Acn44936 Mouse gen
33	89.2	54732	13	ABD33335	Abd33335 Human Can
33	89.2	56153	4	AAJ46793	Aaj46793 Tumour su
33	89.2	58922	13	ABD33407	Abd33407 Human can
33	89.2	86431	6	ABQ74964	Abq74964 Continuation (8 of
33	89.2	96988	3	AAF22290	Aaf22290 BAC conta
33	89.2	110000	6	ABA90521	AbA90521 Continuation (19 o
33	89.2	110000	9	ADB12064	AbD12064 Continuation (7 of
33	89.2	126990	12	ADP13332	Adp13332 Renal cel
33	89.2	193672	10	ADL13570	Adl13570 Osteoarth
33	89.2	194534	12	ADQ97481	Adq97481 Human can
33	89.2	216215	10	ADF69167	Adf69167 Human MP5
33	89.2	217409	11	ACN45150	Acn45150 Human gen
32	86.5	31	2	AAV59931	Aav59931 PCR prime
32	86.5	31	2	AAV58465	Aav58465 Primer fo
32	86.5	31	8	ABX79070	Abx79070 Human ret
32	86.5	121	4	ABA77667	AbA77667 Retinobla

c	77	32	86.5	121	4	ABA77668	Abat7668 Retinobla	150	32	86.5	3555	2	AAV58440	AAV58440 Modified	
	78	32	86.5	398	13	ADX12593	Adx12593 Plant ful	151	32	86.5	3765	11	ADM01807	Adm01807 Human CDN	
	79	32	86.5	466	4	ABL09413	Abi09413 Drosophil	152	32	86.5	3765	14	AEC84737	Aec84737 Human CDN	
c	80	32	86.5	576	12	ADO34573	Ado34573 Human SLI	c	153	3877	12	ADP90661	Adp90661 Mouse ext		
c	81	32	86.5	591	13	ACN60693	Acn60693 Cotton gy	154	32	86.5	4432	13	ADV40792	Adv40792 Rat cardi	
c	82	32	86.5	600	10	ACF68049	Acf68049 Photorhab	155	32	86.5	4579	1	AAN81261	Aan81261 Probe for	
c	83	32	86.5	631	5	ABV50016	Abv50016 Human pro	156	32	86.5	4597	1	AAN81369	Aan81369 Human ret	
c	84	32	86.5	639	10	ADF00608	Adf00608 Bacterial	157	32	86.5	4597	2	AAQ70536	AAq70536 Human ret	
c	85	32	86.5	795	6	AB212201	Ab212201 Arabidops	158	32	86.5	4597	2	AAX04501	Aax04501 Human ret	
c	86	32	86.5	1020	10	ADC92233	Adc92233 E. faeciu	159	32	86.5	4600	13	ADR52909	Adr52909 Drug ther	
c	87	32	86.5	1024	10	ABZ83423	Abz83423 Toxicolog	160	32	86.5	4641	4	ABL16126	Abi16126 Drosophil	
c	88	32	86.5	1056	3	AAZ847383	Aaz847383 Arabidops	161	32	86.5	4740	6	ABK86079	Abk86079 Human ret	
c	89	32	86.5	1063	3	ACA33107	Aac33107 Arabidops	162	32	86.5	4740	10	ADE84952	Ade84952 Farnesyl	
c	90	32	86.5	1125	8	ACA32019	Ac32019 Prokaryot	163	32	86.5	4740	10	ADK67029	Adk67029 Gene #119	
c	91	32	86.5	1161	6	ABL89390	Abi89390 Babesia m	164	32	86.5	4740	12	ADP21395	Adp21395 Gene RB1	
c	92	32	86.5	1161	10	ADE06059	Ade06059 BMNI-rela	165	32	86.5	4740	14	ADV15003	Adv15003 DNA encod	
c	93	32	86.5	1162	6	ABL89383	Abi89383 Babesia m	166	32	86.5	4740	14	ADY19476	Ady19476 DNA encod	
c	94	32	86.5	1162	10	ADE06052	Ade06052 BMNI-rela	167	32	86.5	4740	15	AEF74797	Aef74797 Human pol	
c	95	32	86.5	1248	6	ABL89429	Abi89429 Babesia m	168	32	86.5	4741	12	ACF57516	Acf57516 Human Rb	
c	96	32	86.5	1248	10	ADE06111	Ade06111 BMNI-rela	169	32	86.5	4839	3	AAZ88444	Aaz88444 Human and	
c	97	32	86.5	1304	13	ADT15452	Adt15452 Plant CDN	170	32	86.5	4839	3	AAA29391	Aaa29391 Human ret	
c	98	32	86.5	1775	11	ADP65595	Adp65595 Human alp	171	32	86.5	4839	6	ABL62873	Abi62873 Breast ca	
c	99	32	86.5	1904	13	ADT18553	Adt18553 Plant CDN	172	32	86.5	4839	12	ADP72311	Adp72311 Human Rb	
c	100	32	86.5	2263	14	ACA53600	Aca53600 Prokaryot	173	32	86.5	4839	15	AEF74994	Aef74994 Human pol	
	101	32	86.5	2263	14	AEA22558	Aea22558 Mouse LRM	174	32	86.5	5056	1	AAN90489	Aan90489 CDNA of h	
	102	32	86.5	2466	4	ABL09412	Abi09412 Drosophil	c	175	32	86.5	5430	4	AAS46291	Aas46291 Tumour su
	103	32	86.5	2787	14	AEC21879	Aec21879 Human ret	c	176	32	86.5	5884	6	ABL34164	Abi34164 Human imm
	104	32	86.5	2824	14	ABE55609	Ab555609 Human ret	c	177	32	86.5	6301	6	ABL32052	Abi32052 Human imm
	105	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	c	178	32	86.5	6301	6	ABL32052	Abi32052 Human imm
	106	32	86.5	2994	2	AAQ14545	Aaq14545 Retinobla	c	179	32	86.5	8690	4	ABL29150	Abi29150 Drosophil
	107	32	86.5	2994	2	AAQ40004	Aaa40004 Retinobla	c	180	32	86.5	12988	4	AAS36785	Aas36785 Human car
	108	32	86.5	2994	3	AAZ40287	Aaz40287 Wild type	c	181	32	86.5	12988	10	ADJ08897	Adj08897 Human car
	109	32	86.5	2994	10	ADE21373	Ade21373 Retinobla	c	182	32	86.5	12988	13	ADJ08897	Adj08897 Human car
	110	32	86.5	2994	12	ADF72347	Adf72347 Human ret	c	183	32	86.5	18036	4	AAS36787	Aas36787 Human car
	111	32	86.5	2994	14	ADW20875	Adw20875 Retinobla	c	184	32	86.5	18036	10	ADE47481	Ad47481 Human car
	112	32	86.5	2994	15	AEF64205	Aef64205 Human ret	c	185	32	86.5	18036	13	ADJ08899	Adj08899 Human car
	113	32	86.5	2995	2	AAQ90059	Aaq90059 Retinobla	c	186	32	86.5	18177	1	AAN90490	Aan90490 DNA of hu
	114	32	86.5	2995	2	AAQ86398	Aaq86398 Human Rb1	c	187	32	86.5	18303	2	AAX04502	Aax04502 Human ret
	115	32	86.5	2995	2	AAQ90350	Aaq90350 Human p11	c	188	32	86.5	24993	4	AAK65726	Aak65726 Human imm
	116	32	86.5	2995	2	AAX00737	Aax00737 cDNA enco	c	189	32	86.5	25373	12	ADK16022	Adk16022 Human mam
	117	32	86.5	2995	4	ABL50904	Abi50904 Retinobla	c	190	32	86.5	51469	4	AAK78813	Aak78813 Human imm
	118	32	86.5	2995	4	AH25755	Aah25755 Retinobla	c	191	32	86.5	51469	4	AAK70270	Aak70270 Human imm
	119	32	86.5	2995	4	AH25755	Aah25755 Retinobla	c	192	32	86.5	51469	4	AAK69322	Aak69322 Human imm
	120	32	86.5	2995	9	ACD28570	Ac28570 Human ret	c	193	32	86.5	59001	12	ADH54712	Adh54712 Human VEG
	121	32	86.5	2995	10	ABS57802	Abs57802 cDNA enco	c	194	32	86.5	61020	4	AAS46788	Aas46788 Tumour su
	122	32	86.5	2995	12	ADJ66141	Adj66141 Human ret	c	195	32	86.5	80423	13	ABD32576	Abd32576 Mouse can
	123	32	86.5	2995	12	ADO14562	Ado14562 DNA encod	c	196	32	86.5	92219	13	ABD33589	Abd33589 Murine ca
	124	32	86.5	2995	14	ADM20878	Adm20878 Retinobla	c	197	32	86.5	92219	14	ADZ13328	Adz13328 Murine ca
	125	32	86.5	3089	8	ABX79077	Abx79077 Human ret	c	198	32	86.5	110000	10	ADZ13328	Adz13328 Murine ca
	126	32	86.5	3089	8	ABX79077	Abx79077 Human ret	c	199	32	86.5	110000	10	ADZ13328	Adz13328 Murine ca
	127	32	86.5	3113	8	AAV58445	Aav58445 Modified	c	200	32	86.5	110000	12	ADO34435	Ado34435 1
	128	32	86.5	3116	8	ABX79049	Abx79049 Human ret	c	201	32	86.5	247544	12	ADQ59419	Adq59419 Human can
	129	32	86.5	3218	2	AAV54991	Aav54991 DNA seque	c	202	32	86.5	247544	14	ADZ13712	Adz13712 Murine can
	130	32	86.5	3233	2	AAQ72690	Aaq72690 Retinobla	c	203	32	86.5	247544	14	ADZ13712	Adz13712 Murine can
	131	32	86.5	3244	8	ABX79076	Abx79076 Human ret	c	204	32	86.5	247544	14	ADZ13712	Adz13712 Murine can
	132	32	86.5	3266	2	AAV58444	Aav58444 Modified	c	205	32	86.5	247544	14	ADZ13712	Adz13712 Murine can
	133	32	86.5	3269	8	ABX79078	Abx79078 Human ret	c	206	32	86.5	247544	14	ADZ13712	Adz13712 Murine can
	134	32	86.5	3299	8	ABX79075	Abx79075 Human ret	c	207	32	86.5	247544	14	ADZ13712	Adz13712 Murine can
	135	32	86.5	3299	8	ABX79075	Abx79075 Human ret	c	208	32	86.5	247544	14	ADZ13712	Adz13712 Murine can
	136	32	86.5	3353	8	ABX79082	Abx79082 Human ret	c	209	32	86.5	247544	14	ADZ13712	Adz13712 Murine can
	137	32	86.5	3359	8	ABX79083	Abx79083 Human ret	c	210	32	86.5	247544	14	ADZ13712	Adz13712 Murine can
	138	32	86.5	3368	8	ABX79074	Abx79074 Human ret	c	211	32	86.5	247544	14	ADZ13712	Adz13712 Murine can
	139	32	86.5	3377	2	AAV58450	Aav58450 Modified	c	212	32	86.5	247544	14	ADZ13712	Adz13712 Murine can
	140	32	86.5	3383	2	AAV58451	Aav58451 Modified	c	213	32	86.5	247544	14	ADZ13712	Adz13712 Murine can
	141	32	86.5	3392	2	AAV58442	Aav58442 Modified	c	214	32	86.5	247544	14	ADZ13712	Adz13712 Murine can
	142	32	86.5	3433	8	ABX79073	Abx79073 Human ret	c	215	32	86.5	247544	14	ADZ13712	Adz13712 Murine can
	143	32	86.5	3437	8	ABX79079	Abx79079 Human ret	c	216	32	86.5	247544	14	ADZ13712	Adz13712 Murine can
	144	32	86.5	3455	2	AAV58441	Aav58441 Modified	c	217	32	86.5	247544	14	ADZ13712	Adz13712 Murine can
	145	32	86.5	3461	2	AAV58447	Aav58447 Modified	c	218	32	86.5	247544	14	ADZ13712	Adz13712 Murine can
	146	32	86.5	3532	8	ABX79084	Abx79084 Human ret	c	219	32	86.5	247544	14	ADZ13712	Adz13712 Murine can
	147	32	86.5	3533	8	ABX79048	Abx79048 Human ret	c	220	32	86.5	247544	14	ADZ13712	Adz13712 Murine can
	148	32	86.5	3554	2	AAV58452	Aav58452 Modified	c	221	32	86.5	247544	14	ADZ13712	Adz13712 Murine can
	149	32	86.5	3555	2	AAV54990	Aav54990 DNA seque	c	222	32	86.5	247544	14	ADZ13712	Adz13712 Murine can
	150	32	86.5	3555	2	AAV54990	Aav54990 DNA seque	c	222	32	86.5	247544	14	ADZ13712	Adz13712 Murine can